

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:34:13 ; Search time 110.536 Seconds  
(without alignments)  
922.194 Million cell updates/sec

Title: US-09-847-208b-3  
Perfect score: 1260  
Sequence: 1 EPKSCDKTHTPCCPAPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: geneseqp1980a.\*  
2: geneseqp1990a.\*  
3: geneseqp2000a.\*  
4: geneseqp2001a.\*  
5: geneseqp2002a.\*  
6: geneseqp2003a.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004a.\*  
9: geneseqp2005a.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1260	100.0	232	AA019665	AA019665 Human IgG
2	1260	100.0	330	AA019664	AA019664 Human IgG
3	1260	100.0	569	AA019668	AA019668 GE2 fusio
4	1232	97.8	232	AD287506	AD287506 Human IgG
5	1228	97.5	330	AD269628	AD269628 Human IgG
6	1225	97.2	232	AAW26232	AAW26232 Human IgG
7	1225	97.2	232	AAE28690	AAE28690 Human IgG
8	1225	97.2	232	AAE28690	AAE28690 Human IgG
9	1225	97.2	232	AAE28690	AAE28690 Human IgG
10	1225	97.2	232	AAE15347	AAE15347 Human par
11	1225	97.2	232	AAE26272	AAE26272 Human IgG
12	1225	97.2	232	ADJ65991	ADJ65991 Herpes vi
13	1225	97.2	232	ADJ57512	ADJ57512 Human IgG
14	1225	97.2	232	ADU51146	ADU51146 Human sp1
15	1225	97.2	232	ADR48992	ADR48992 Human IgG
16	1225	97.2	232	ADW39127	ADW39127 Novel TNF
17	1225	97.2	232	ADV91799	ADV91799 Human GCS
18	1225	97.2	232	ADV99720	ADV99720 Human IgG
19	1225	97.2	232	ADY55884	ADY55884 Human IgG
20	1225	97.2	232	ADZ86538	ADZ86538 Human IgG
21	1225	97.2	232	AEA18941	AEA18941 Human IgG
22	1225	97.2	232	AEA88761	AEA88761 Human IgG
23	1225	97.2	233	ABB09463	ABB09463 Human IgG
24	1225	97.2	234	ADY22146	ADY22146 Human imm

25	1225	97.2	235	6	ABJ38647	ABJ38647 pCXFc pro
26	1225	97.2	235	6	ADA89055	ADA89055 Plasmid p
27	1225	97.2	235	7	ADD25647	ADD25647 Binding d
28	1225	97.2	235	7	ADG74307	ADG74307 Fibroblas
29	1225	97.2	235	9	ADY21627	ADY21627 Human IgG
30	1225	97.2	247	5	AAE26274	AAE26274 Human bet
31	1225	97.2	251	6	ABB81490	ABB81490 Human imm
32	1225	97.2	251	6	AAE35214	AAE35214 Human wil
33	1225	97.2	259	2	AAAY24154	AAAY24154 Protein f
34	1225	97.2	267	5	AAE26273	AAE26273 Human tPA
35	1225	97.2	269	8	ADJ52120	ADJ52120 CHI delet
36	1225	97.2	285	9	AEA89551	AEA89551 Human imm
37	1225	97.2	287	4	AAAB47590	AAAB47590 Fusion pr
38	1225	97.2	288	9	AEA89541	AEA89541 Human imm
39	1225	97.2	329	2	AAAR91806	AAAR91806 Human imm
40	1225	97.2	329	8	ADP56389	ADP56389 Human PRO
41	1225	97.2	329	8	ADS82579	ADS82579 Human IgG
42	1225	97.2	330	4	AAAB04071	AAAB04071 Zcytor 10
43	1225	97.2	330	5	AAAM47856	AAAM47856 Human Ig-
44	1225	97.2	330	5	AAE21960	AAE21960 Human dea
45	1225	97.2	330	5	ABB81641	ABB81641 Human IgG

## ALIGNMENTS

RESULT 1  
AA019665  
ID AA019665 standard; protein; 232 AA.  
XX  
AC AA019665;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
DE Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.  
XX  
KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiaethmatic; antiallergic; antiinflammatory; dermatological;  
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;  
KW hinge-CH2-CH3 region.  
XX  
OS Homo sapiens.  
XX  
FN WO200288317-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013527.  
XX  
PR 01-MAY-2001; 2001US-00847208.  
PR 24-OCT-2001; 2001US-00000439.  
XX  
(REGC ) UNIV CALIFORNIA.  
XX  
PI Saxon A, Zhang K, Zhu D;  
XX  
WPI; 2003-103456/09.  
XX  
New fusion molecules comprising polypeptide sequences that bind to IgG  
inhibitory receptor and native IGE receptor, useful for treating IgG-  
mediated hypersensitivity reactions, e.g. asthma or allergies, or  
autoimmune diseases.  
XX  
Claim 19; Fig 3; 116pp; English.  
XX  
The present invention relates to a fusion molecule comprising a first  
polypeptide sequence capable of specific binding to a native IgG  
inhibitory receptor consisting of an immune receptor tyrosine-based  
inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
functionally connected to a second polypeptide sequence capable of  
specific binding directly or indirectly to a native IGE receptor  
(Fc epsilonR). Also provided are nucleotide sequences encoding such a

CC fusion protein. The fusion molecules and compositions are useful for  
 CC treating an IGE-mediated biological response, preferably an IGE-mediated  
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
 CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
 CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgG1  
 CC heavy chain constant region hinge-CH2-CH3 portion  
 XX  
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1260; DB 6; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-91;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120  
 DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 232

RESULT 2  
 AAO19664  
 ID AAO19664 standard; protein; 330 AA.  
 XX  
 AC AAO19664;

XX 28-MAR-2003 (first entry)  
 XX Human IgG1 heavy chain constant region.  
 XX  
 XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
 KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological;  
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.  
 XX  
 OS Homo sapiens.

XX WO200288317-A2.  
 XX 07-NOV-2002.  
 XX 01-MAY-2002; 2002WO-US013527.  
 XX 01-MAY-2001; 2001US-00847208.  
 XX 24-OCT-2001; 2001US-00000439.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Saxon A, Zhang K, Zhu D;  
 XX WPI; 2003-103456/09.  
 XX New fusion molecules comprising polypeptide sequences that bind to IgG  
 PT inhibitory receptor and native IGE receptor, useful for treating IGE-  
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
 PT autoimmune diseases.  
 XX Claim 64; Fig 2; 116pp; English.  
 XX The present invention relates to a fusion molecule comprising a first

CC polypeptide sequence capable of specific binding to a native IgG  
 CC inhibitory receptor consisting of an immune receptor tyrosine-based  
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
 CC functionally connected to a second polypeptide sequence capable of  
 CC specific binding directly or indirectly to a native IGE receptor  
 CC (Fc epsilonR). Also provided are nucleotide sequences encoding such a  
 CC fusion protein. The fusion molecules and compositions are useful for  
 CC treating an IGE-mediated biological response, preferably an IGE-mediated  
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
 CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
 CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgG1  
 CC heavy chain constant region  
 XX

SQ Sequence 330 AA;  
 Query Match 100.0%; Score 1260; DB 6; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-91;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 120  
 DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNGKEYCKVSNKALPAPIEKT 218  
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 232  
 DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 330

RESULT 3  
 AAO19668  
 ID AAO19668 standard; protein; 569 AA.  
 XX  
 AC AAO19668;  
 XX 28-MAR-2003 (first entry)  
 XX GE2 fusion protein for use in treating immune diseases.  
 XX  
 XX Human; IgE; immunoglobulin E; immunotherapy; immune disease;  
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
 KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological; GE2;  
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;  
 KW fusion protein.  
 XX  
 OS Synthetic.  
 OS Unidentified.  
 XX WO200288317-A2.  
 XX 07-NOV-2002.  
 XX 01-MAY-2002; 2002WO-US013527.  
 XX 01-MAY-2001; 2001US-00847208.  
 XX 24-OCT-2001; 2001US-00000439.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX Saxon A, Zhang K, Zhu D;  
 XX WPI; 2003-103456/09.

PT New fusion molecules comprising polypeptide sequences that bind to IgG  
PT inhibitory receptor and native IgE receptor, useful for treating IgE-  
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
PT autoimmune diseases.  
XX  
PS Claim 35; Fig 7; 116pp; English.  
XX  
CC The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IgG  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IgE receptor  
CC (Fcεsilon2). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IgE-mediated biological response, preferably an IgE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is a gammahinge-  
CC CHgamma2-CHgamma3-(Gly4Ser)3-CHepsilon2-CHepsilon3-CHepsilon3 fusion  
CC protein (designated GE2) of the invention  
XX  
SQ Sequence 569 AA;

Query Match 100.0%; Score 1260; DB 6; Length 569;  
Best Local Similarity 100.0%; Pred. No. 9.7e-91;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKCKVSNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVWHEALHNHYQOQSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVWHEALHNHYQOQSLSLSPGK 232

RESULT 4  
ADZ87506  
ID ADZ87506 standard; protein; 232 AA.  
XX  
AC ADZ87506;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Human IgG1 protein region SeqID33.  
XX  
DE protein engineering; immunoglobulin; cytostatic; cancer.  
XX  
KW Homo sapiens.  
XX  
OS WO2005042573-A1.  
XX  
PN 12-MAY-2005.  
XX  
PD 21-OCT-2004; 2004WO-US034680.  
XX  
PF 24-OCT-2003; 2003US-0514198P.  
XX  
PR 12-NOV-2003; 2003US-0519822P.  
XX  
XX (DAND ) DANA FARBER CANCER INST INC.  
PA (ILEX-) ILEX PROD INC.

XX Kharbanda S, Kufe DW;  
PI WPI; 2005-346855/35.  
XX N-PSDB; ADZ87507.  
DR  
XX  
PT MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an  
PT immunoglobulin FC polypeptide or an albumin polypeptide, useful for  
PT treating cancer.  
XX  
PS Disclosure; SEQ ID NO 33; 82pp; English.  
XX  
CC This invention relates to a novel MUC1 chimeric protein which comprises a  
CC first polypeptide sequence and a second polypeptide sequence, where the  
CC first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide,  
CC and the second polypeptide sequence is a human immunoglobulin FC  
CC polypeptide or a human albumin polypeptide. The invention may be useful  
CC for the development of compounds with a cytostatic activity acting as  
CC MUC1 antagonists or CD227 antagonists. The MUC1 chimeric protein is  
CC useful in preparing a composition for treating cancer. The present  
CC sequence is that of a protein which was used during the development of  
CC the novel MUC1 chimeric protein of the invention.  
XX  
SQ Sequence 232 AA;

Query Match 97.8%; Score 1232; DB 9; Length 232;  
Best Local Similarity 97.4%; Pred. No. 5.4e-89;  
Matches 226; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKCKVSNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVWHEALHNHYQOQSLSLSPGK 232  
DB 181 PVLDSVGSFFLYSKLTVDKSRWQOGNPFSCSVWHEALHNHYQOQSLSLSPGK 232

RESULT 5  
ADZ69628  
ID ADZ69628 standard; protein; 330 AA.  
XX  
AC ADZ69628;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Human IgG1 heavy chain constant region, mutant L314M.  
XX  
DE Heavy chain constant region; antibody engineering; protein engineering;  
XX immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasia;  
XX autoimmune disease; immunosuppressive; immune disorder.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 197  
ET /note= "Wild-type Leu substituted by Met"  
XX  
PN WO2005037867-A1.  
XX  
XX 28-APR-2005.  
XX  
XX 15-OCT-2004; 2004WO-US034440.  
XX

PR 15-OCT-2003; 2003US-0511697P.  
PR 14-APR-2004; 2004US-0562627P.  
XX (PROT-) PROTEIN DESIGN LABS INC.  
XX Hinton PR, Tsurushita N;  
XX WPI; 2005-315693/32.  
XX New modified Fc-fusion protein where at least one amino acid residue from  
PT the heavy chain constant region, useful for studying protein function in  
PT vitro and in vivo and as potential therapeutic and diagnostic agents.  
XX  
XX Claim 21; SEQ ID NO 29; 170pp; English.  
XX  
XX The invention relates to a modified Fc-fusion protein where at least one  
CC amino acid residue from the heavy chain constant region selected from  
CC residues 250, 314, and 428 (Kabat numbering) is different from that  
CC present in the unmodified Fc-fusion protein. Also included are an Fc-  
CC fusion protein comprising an Fc region substantially identical to that of  
CC a naturally occurring class IgG antibody, a modified Fc-fusion protein  
CC with an in vivo mean elimination half-life at least about 1.3-fold longer  
CC than that of the corresponding unmodified Fc-fusion protein, a modified  
CC IgG class antibody fragment (comprising a heavy chain constant region or  
CC Fc-region where at least one amino acid residue selected from the group  
CC consisting of residues 250, 314, and 428 is different from that present  
CC in the unmodified IgG class antibody), an isolated polynucleotide  
CC molecule encoding a polypeptide comprising a sequence at least 90%  
CC identical to a sequence selected from ADZ69600-ADZ69656, an isolated  
CC polypeptide comprising an amino acid sequence at least 90% identical to a  
CC sequence selected from ADZ69600-ADZ69656, a method for altering FcRn  
CC binding affinity/serum half-life of an Fc-fusion protein (comprising  
CC selecting at least one amino acid residue as cited above, and  
CC substituting the selected residue(s) with an amino acid different from  
CC that present in the Fc-fusion protein) and a method of producing a  
CC modified Fc-fusion protein with an altered binding affinity for  
CC FcRn/alteted serum half-life as compared with the unmodified Fc-fusion  
CC protein (comprising preparing an expression vector comprising a suitable  
CC promoter operably linked to DNA encoding at least a constant region of an  
CC IgG heavy chain, transforming host cells with the vector and culturing  
CC the transformed host cells to produce the modified IgG Fc fusion  
CC protein). The modified antibody has a higher affinity for FcRn at pH 6.0  
CC than at pH 8.0. The fusion proteins are useful for studying protein  
CC function in vitro and in vivo and as potential therapeutic and diagnostic  
CC agents. The present sequence represents a human IgG1 heavy chain constant  
CC region with an amino acid substitution at residue 250, 314 or 428 (Kabat  
CC numbering, the actual residue that is mutated is covered in the feature  
CC table).  
XX  
SQ Sequence 330 AA;

Query Match 97.5%; Score 1228; DB 9; Length 330;  
Best Local Similarity 97.4%; Pred. No. 1.7e-88;  
Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHONMNGKEYCKVSKNKAIPAPIEKT 120  
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODMNGKEYCKVSKNKAIPAPIEKT 218  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYQQRSLSPGK 232  
Db 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYTKLSLSPGK 330

RESULT 6

AAW26232  
ID AAW26232 standard; protein; 232 AA.  
XX  
XX AAW26232;  
XX AC  
XX DT 16-MAR-1998 (first entry)  
XX DE Human IgG1 hinge/Fc region.  
XX KW Fusion protein; hydrophilic spacer; recombinant; expression system;  
KW carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.  
XX OS Homo sapiens.  
XX PN WO9728272-A1.  
XX PD 07-AUG-1997.  
XX PF 31-JAN-1997; 97WO-US001470.  
XX PR 31-JAN-1996; 96US-00595043.  
XX PA (TECH-) TECHNOLOGENE INC.  
XX PI Sgarlato GD;  
XX WPI; 1997-402624/37.  
DR N-PSDB; AAT80158.  
XX PT Recombinant protein expression system for fusion protein production -  
PT useful for high quantity production of authentic recombinant proteins.  
XX Example 3; Page 133-134; 194pp; English.  
XX A novel recombinant vector has been developed which comprises a  
CC nucleotide sequence encoding a fusion protein. The fusion protein  
CC comprises three domains joined together in order, from N-terminus to C-  
CC terminus, of a first domain comprising a protein of interest, a second  
CC domain comprising a hydrophilic spacer and an affinity domain, each  
CC domain comprising amino acid residues. The present sequence represents  
CC the hinge/Fc region of human IgG1, used in example 3 of the present  
CC invention. The recombinant vector is used for the production of authentic  
CC recombinant proteins of interest. The method of the invention is useful  
CC for the expression of fusion proteins capable of isolation by affinity  
CC chromatography in pro- or eukaryotic cells. This method allows for the  
CC efficient cleavage and generation of authentic proteins of interest that  
CC do not contain extraneous (i.e. non-naturally occurring) amino acids  
XX  
SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 2; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.9e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHONMNGKEYCKVSKNKAIPAPIEKT 120  
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHODMNGKEYCKVSKNKAIPAPIEKT 120  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Db 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYQQRSLSPGK 232  
Db 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSVMHREALHNNHYTKLSLSPGK 232

RESULT 7  
AAB28690



ID AAB28690 standard; protein; 232 AA.  
 XX AC AAB28690;  
 XX DT 14-FEB-2001 (first entry)  
 XX DE Human IgGammal hinge, CH2 and CH3 regions.  
 XX KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;  
 KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;  
 KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;  
 KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;  
 KW transplant rejection; cardiovascular disease; arteriosclerosis;  
 KW IgGammal.  
 XX OS Homo sapiens.  
 XX PN WO200063253-A1.  
 XX PD 26-OCT-2000.  
 XX PF 24-MAR-2000; 2000WO-US008004.  
 XX PR 16-APR-1999; 99US-00293245.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Hsu H, Meng S;  
 XX DR WPI; 2000-665240/64.  
 XX PT Fusion protein of AGP-1 protein and an Fc region, used to treat  
 PT proliferative disorders, immune disorders, and virally-induced disorders.  
 XX PS Claim 2; Fig 1; 93pp; English.  
 XX CC The present sequence was used in the production of AGP-1 fusion proteins.  
 CC AGP-1 is a type II transmembrane protein. The fusion proteins comprise an  
 CC Fc immunoglobulin region fused to the N-terminal portion of the AGP-1  
 CC protein. The fusion proteins can be used to induce apoptosis in a tissue,  
 CC and to treat proliferative disorders, immune disorders, or virally-  
 CC induced disorders. The proliferative disorders include cancers, such as  
 CC breast, prostate, lung or colon cancer. The viral infections include  
 CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune  
 CC disorders may be autoimmune disorders or transplant rejection.  
 CC Cardiovascular diseases such as arteriosclerosis may also be treated. The  
 CC AGP-1 containing fusion proteins have increased biological activity  
 CC compared to the soluble AGP-1 proteins used in prior art therapies  
 XX SQ Sequence 232 AA;  
 Query Match 97.2%; Score 1225; DB 3; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLTQHNWNGKEYCKVSNKALPAPIEKT 120  
 DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLTQHNWNGKEYCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

RESULT 8

AAB80897  
 ID AAB80897 standard; protein; 232 AA.  
 XX AC AAB80897;  
 XX DT 31-MAY-2001 (first entry)  
 XX DE Human IgGammal hinge, CH2 and CH3 regions.  
 XX KW Human; IgGammal; anticancer; Antimetastatic; Osteogenic;  
 KW lytic bone disease; multiple myeloma; immunoglobulin;  
 KW osteoclastic bone metastasis; OPG; osteoprotegerin;  
 KW osteoclast formation inhibition; bone resorption inhibition.  
 XX OS Homo sapiens.  
 XX PN WO200117543-A2.  
 XX PD 15-MAR-2001.  
 XX PF 18-AUG-2000; 2000WO-US022806.  
 XX PR 03-SEP-1999; 99US-00389545.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Dunstan CR;  
 XX DR WPI; 2001-265936/27.  
 XX PT Preventing or treating lytic bone diseases, particularly associated with  
 PT cancer or metastasis, by administering an osteoprotegerin polypeptide.  
 XX PS Disclosure; Fig 1; 87pp; English.  
 XX CC The present invention relates to a method for the prevention or treatment  
 CC of lytic bone disease or multiple myeloma. Also the method can be used  
 CC for preventing metastasis of cancer to bone or osteosclerotic bone  
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)  
 CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-  
 CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)  
 CC by blocking differentiation from monocytes/macrophage precursors. The  
 CC present sequence is the hinge, CH2 and CH3 regions of human IgGammal.  
 CC This sequence can be used to generate fusion proteins of OPG and  
 CC immunoglobulin, for use in the present invention. The generated fusion  
 CC proteins can exhibit increased circulating half-lives and slower  
 CC clearance times, thereby providing a more sustained activity  
 XX SQ Sequence 232 AA;  
 Query Match 97.2%; Score 1225; DB 4; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLTQHNWNGKEYCKVSNKALPAPIEKT 120  
 DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLTQHNWNGKEYCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

RESULT 9  
 AAY72915

AAE15347 standard; protein; 232 AA.  
AAE15347;  
09-APR-2002 (first entry)  
Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.  
Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;  
cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.  
Homo sapiens.  
WO200181405-A2.  
01-NOV-2001.  
19-APR-2001; 2001WO-US012836.  
21-APR-2000; 2000US-00559001.  
(AMGE-) AMGEN INC.  
Egrie JC, Elliott SG, Browne JK, Sitney KC;  
WPI; 2002-034433/04.  
Increasing and maintaining hematocrit in mammal suffering from anemia,  
comprising administering hyperglycosylated analog of erythropoietin less  
frequently and at lower molar amount of recombinant human erythropoietin.  
Example 1; Fig 10; 95pp; English.  
The invention relates to a method for increasing and maintaining  
haematocrit in a mammal. The method comprises administering a  
hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical  
composition, less frequently than an equivalent molar amount of and at a  
lower molar amount than recombinant human Epo (rHuEpo) to obtain a  
comparable target haematocrit. Epo is a glycoprotein hormone necessary  
for the maturation of erythroid progenitor cells into erythrocytes. Human  
Epo analogue is useful for raising and maintaining haematocrit to a  
comparable target haematocrit in a mammal suffering from anaemia  
associated with a decline or loss of kidney function, myelosuppressive  
therapy comprising chemotherapeutic or anti-viral drugs or associated  
with excessive blood loss during surgical procedures, and in cancer  
condition. The present sequence is human immunoglobulin G (IgG) gamma 1  
constant heavy chain (CH2, CH3) hinge region used to construct Epo  
hyperglycosylated analogue fusion protein

AAE15347 standard; protein; 232 AA.  
AAE15347;  
13-JUN-2001 (first entry)  
Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.  
Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
periodontal.  
Homo sapiens.  
WO200118203-A1.  
15-MAR-2001.  
18-AUG-2000; 2000WO-US022797.  
03-SEP-1999; 99US-00389782.  
(AMGE-) AMGEN INC.  
Dunstan CR, Wooden SK, Mann MB;  
WPI; 2001-244572/25.  
Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
by e.g. osteoporosis, Paget's disease and osteomyelitis.  
Claim 3; Fig 1; 119pp; English.  
The patent discloses fusion protein comprising human osteoprotegerin  
(OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively  
regulates formation of osteoclasts in vitro and in vivo. It blocks the  
differentiation of osteoclasts from monocyte or macrophage precursors and  
the reabsorption of bone. The OPG-Fc fusion protein is administered for  
the treatment of bone loss resulting from osteoporosis, Paget's disease,  
osteomyelitis, hypercalcaemia, osteopenia associated with surgery or  
steroid administration, osteonecrosis, bone loss due to rheumatoid  
arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic  
loosening. The present sequence is partial human immunoglobulin G (Ig G)  
1 protein comprising the hinge and heavy chain constant regions CH2 and  
CH3

AAE15347 standard; protein; 232 AA.  
AAE15347;  
13-JUN-2001 (first entry)  
Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.  
Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
periodontal.  
Homo sapiens.  
WO200118203-A1.  
15-MAR-2001.  
18-AUG-2000; 2000WO-US022797.  
03-SEP-1999; 99US-00389782.  
(AMGE-) AMGEN INC.  
Dunstan CR, Wooden SK, Mann MB;  
WPI; 2001-244572/25.  
Osteoprotegerin-Fc protein fusions useful for treating bone loss caused  
by e.g. osteoporosis, Paget's disease and osteomyelitis.  
Claim 3; Fig 1; 119pp; English.  
The patent discloses fusion protein comprising human osteoprotegerin  
(OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively  
regulates formation of osteoclasts in vitro and in vivo. It blocks the  
differentiation of osteoclasts from monocyte or macrophage precursors and  
the reabsorption of bone. The OPG-Fc fusion protein is administered for  
the treatment of bone loss resulting from osteoporosis, Paget's disease,  
osteomyelitis, hypercalcaemia, osteopenia associated with surgery or  
steroid administration, osteonecrosis, bone loss due to rheumatoid  
arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic  
loosening. The present sequence is partial human immunoglobulin G (Ig G)  
1 protein comprising the hinge and heavy chain constant regions CH2 and  
CH3

Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 1.9e-88;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
QY 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPGK 232  
DB 181 PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSVWHEALHNHYTQKSLSLSPGK 232

RESULT 10  
AAE15347





CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line  
 CC producing the HuEPO-L-vFc fusion protein in its growth medium in excess  
 CC of 30  $\mu$ mol/l per million cells in a 24 hour period. The human IgG Fc  
 CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from  
 CC IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,  
 CC the IgG Fc contains amino acid mutations to attenuate effector functions,  
 CC a flexible peptide linker containing 20 or fewer amino acids is present  
 CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vFc fusion  
 CC protein exhibits in vitro biological activity similar to or higher than  
 CC that of HuEPO on a molar basis. Preferred Method: Making a recombinant  
 CC fusion protein comprising HuEPO, a flexible peptide linker, and a human  
 CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the  
 CC cell line where the recombinant protein is expressed in its growth medium  
 CC in excess of 10  $\mu$ mol/l per million cells in a 24 hour period; and  
 CC purifying the expressed protein from (b), where the recombinant fusion  
 CC protein exhibits in vitro biological activity similar to or higher than  
 CC that of HuEPO on a molar basis. Antianemic; Nephrotropic. No biological  
 CC data given. None given. Administration can be through subcutaneous or  
 CC intravenous route. No dosage given. The recombinant HuEPO-L-vFc fusion  
 CC protein is useful for treating patients with chronic anemia due to renal  
 CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for  
 CC HIV infection, or myelodysplastic syndrome. It is also useful in the  
 CC treatment of renal failure. A fusion protein was assembled from several  
 CC DNA segments. To obtain the gene encoding the leader peptide and mature  
 CC protein of human erythropoietin (EPO), cDNA library of human fetal liver  
 CC or kidney was used as the template in polymerase chain reaction (PCR).  
 CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a  
 CC restriction enzyme cleavage site is used as the 5' oligonucleotide  
 CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon  
 CC and incorporates a BamHI site. The resulting DNA fragments of  
 CC approximately 600 bp were inserted into a holding vector such as pUC19 at  
 CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the  
 CC human EPO gene was confirmed by DNA sequencing.

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIKT 120  
 DB 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIKT 120  
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232  
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232

RESULT 15

ADU51146  
 ID ADU51146 standard; protein; 232 AA.

XX AC ADU51146;

XX DT 27-JAN-2005 (first entry)

XX DE Human spleen-expressed receptor-related solubility-promoting protein.

XX KW immunosuppressive; cytostatic; antiinflammatory; immune modulation;  
 KW intercellular communication; autoimmune disease; cancer; neoplasm;  
 KW transplant rejection; immune disorder; inflammation; gene therapy.

OS Homo sapiens.

XX

PN WO2004096976-A2.

XX PD 11-NOV-2004.

XX PF 29-APR-2004; 2004WO-EP004562.

XX PR 30-APR-2003; 2003US-0467206P.

XX PA (NOVS ) NOVARTIS AG.

XX PA (NOVS ) NOVARTIS PHARMA GMBH.

XX PA (SCRI ) SCRIPPS RES INST.

XX PI Kaye J, Wilkinson B;

XX DR WPI; 2004-804740/79.

XX New purified spleen expressed (SPEX) polypeptide useful for modulating  
 PT lymphocyte activation and the immune response in disorders including  
 PT autoimmunity, cancer, transplant rejection and inflammation.

PS Disclosure; SEQ ID NO 97; 98pp; English.

XX The invention relates to a novel purified polypeptide comprising any of  
 CC SEQ ID Nos: 3, 7, 9, 11, 45 or 88, or an amino acid sequence that is 95%  
 CC or more identical to the amino acid sequences and which includes an  
 CC immunoglobulin like domain structure. The polypeptide of the invention  
 CC demonstrates immunosuppressive, cytostatic and antiinflammatory  
 CC activities and is a spleen-expressed (SPEX) polypeptide. The methods and  
 CC compositions of the present invention may be useful for modulating  
 CC lymphocyte activation and the immune response in a variety of conditions  
 CC including autoimmunity, cancer, transplant rejection and inflammation.  
 CC Such modulation may be achieved via the use of gene therapy. The current  
 CC sequence is that of the human spleen-expressed (SPEX) receptor-related  
 CC solubility-promoting protein of the invention.

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIKT 120  
 DB 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLHQNMMNGKEYCKVSNKALPAPIKT 120  
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232  
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232

Search completed: November 30, 2005, 00:51:22

Job time : 113.536 secs

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Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),  
igen Primärstruktur.  
A;Reference number: A91668; MUID:77070269; PMID:826475  
A;Contents: myeloma protein Nie  
A;Accession: B91668  
A;Molecule type: protein  
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A;Cross-references: UNIPARC:UPI000017378F  
A;Note: this sequence has the Gln(17) and Gln(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A;Title: Die Primärstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL  
A;Reference number: A91723; MUID:83289131; PMID:6884994  
A;Contents: myeloma protein KOL; disulfide bonds  
A;Accession: A91723  
A;Molecule type: protein  
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A;Cross-references: UNIPARC:UPI0000173790  
A;Note: this sequence has the Gln(3) and Gln(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A;Reference number: A90565; MUID:71064027; PMID:4923144  
A;Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A;Reference number: A91667; MUID:77070267; PMID:1002129  
A;Contents: annotation; disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG1  
A;Cross-references: GDB:120085; OMIM:147100  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 114/1; 224/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;137-206/Domain: immunoglobulin homology <IM2>  
F;243-310/Domain: immunoglobulin homology <IM3>  
F;27-83,144-204,250-308/Disulfide bonds: #status experimental  
F;103/Disulfide bonds: interchain (to light chain) #status experimental  
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 97.2%; Score 1225; DB 1; Length 330;  
Best Local Similarity 97.0%; Pred. No. 1.7e-85;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKTHCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 120  
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 218  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278  
QY 181 PVLDSGVSFFLYSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 232  
Db 279 PVLDSGVSFFLYSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330  
RESULT 2  
S69339  
Ig heavy chain v region precursor - human  
C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C;Accession: S69339; S72664  
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A;Reference number: S69339; MUID:95262687; PMID:7744049  
A;Accession: S69339  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <KHA>  
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695  
R;Khamlichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S72664  
A;Accession: S72664  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140, 'C', 142-374 <KH2>  
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
Query Match 96.7%; Score 1219; DB 2; Length 374;  
Best Local Similarity 96.1%; Pred. No. 5.5e-85;  
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 143 EPKSCDKTHCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 120  
Db 203 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 262  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Db 263 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 322  
QY 181 PVLDSGVSFFLYSKLTVDKSRWQGNVFSCSVNHEALHNHYQORSLSLSPGK 232  
Db 323 PVLDSGVSFFLYSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 374  
RESULT 3  
S31866  
Ig gamma-1 chain C region - synthetic  
C;Species: synthetic  
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C;Accession: S31866  
R;Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A;Description: Screening method for protein-protein interactions of cloned gene products.  
A;Reference number: S31866  
A;Accession: S31866  
A;Molecule type: mRNA  
A;Residues: 1-255 <FIL>  
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:  
C;Keywords: immunoglobulin  
F;1-22/Region: Escherichia coli outer membrane protein A precursor  
F;23-255/Region: human Ig gamma-1 chain C region  
Query Match 96.6%; Score 1217; DB 4; Length 255;  
Best Local Similarity 96.6%; Pred. No. 4.9e-85;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 24 EPKSCDKTHCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 120  
Db 84 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVCKVSNKALPAPIEKT 143





A;Cross-references: UNIPARC:UPI0000173797  
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co  
A;Note: the sequence of residues 42-76 was taken from the reference that follows  
R;Michaelsen, T.E.; Frangione, B.; Franklin, E.C.  
J. Biol. Chem. 252, 883-889, 1977  
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
A;Reference number: A92219; MUID:77118561; PMID:402363  
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein w  
A;Accession: A92219  
A;Molecule type: protein  
A;Residues: 12-97 <MIC>  
A;Cross-references: UNIPARC:UPI0000173798  
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
idue segment (12-28)  
R;Wolfe, J.; Frangione, B.; Prell, F.; Franklin, E.C.  
Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
A;Reference number: A90198; MUID:77021516; PMID:823945  
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues  
A;Accession: A90198  
A;Molecule type: protein  
A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>  
A;Cross-references: UNIPARC:UPI0000173799  
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;  
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion  
A;Reference number: A93915; MUID:82247835; PMID:6808505  
A;Contents: heavy chain disease protein Omm  
A;Accession: A93915  
A;Molecule type: mRNA  
A;Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C;  
A;Note: a carboxyl-terminal Lys is removed posttranslationally  
A;Note: this sequence may represent an allelic form or another gamma chain subclass  
C;Comment: The heavy chain disease protein wis is shown.  
C;Genetics:  
A;Gene: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 14q32.33-14q32.33  
A;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid  
F;203-270/Domain: immunoglobulin homology <IMM>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 89.18; Score 1123; DB 1; Length 289;  
Best Local Similarity 88.3%; Pred. No. 7.5e-78;  
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;  
QY 1 EPKSCDTHCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 59 EPKSCDTPPCPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVQF 118  
QY 61 NWYVDGVEHVNVKTPREEQNSTYRVSVLTVLHQMNGMKYCKVSNKALPAPIEKT 120  
Db 119 KWIYDGVQVHNAKTKPEQQFNSTFRVSVLTVLHQNLDGKYEYCKVSNKALPAPIEKT 178  
QY 121 ISKAKVOPREPOVYTLPPSRDELTKQVSLTCLVKGYPSDIAVWESNQPENNYKTP 180  
Db 179 ISKTKGPREPQVYTLPPSRDEMTKNQVSLTCLVKGYPSDIAVWESSQPENNYNTP 238  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSSVMHEALHNHQQRSLSLSPG 231  
Db 239 PMLDSGSPFLYSLKTLVDKSRWQGNIFSCSVMHEALHNHPTQKLSLSFG 289  
RESULT 8  
G2HU  
Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain cont  
A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-336 <ELL>  
A;Cross-references: UNIPROT:P01859; UNIPARC:UPI00003BFCC; GB:V00554; GB:J00230; NID:g32;  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A;Reference number: A92809; MUID:81007873; PMID:6774012  
A;Contents: myeloma protein TII  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A;Cross-references: UNIPARC:UPI0000173791  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a h  
A;Reference number: A90752; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-1  
A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g  
A;Reference number: A93132; MUID:80114419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
A;Cross-references: UNIPARC:UPI0000173794  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;133-202/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F;102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 87.9%; Score 1107; DB 1; Length 326;



QY 45 TCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYNSTYRVSVLTVLHQNWMNGKEY 104  
 Db 136 TCVVVDVSDPDPEVKFQWYINNEQVTRARPLEQQFNSTIRVSVLTPIHQDWLGRKEF 195  
 QY 105 KCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAV 164  
 Db 196 KCKVHNKALPAPIEKTISKARGQLPKVYTMGPPEELSSRSVLTCLMNGEYPSDISV 255  
 QY 165 EWSNGQPNENYKTPPVLSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQR 224  
 Db 256 EWEKNGKAEDNYKTPPAVLSDGSGFLYLNKLSVPTSEWQRGDVFTCSVMHEALHNHYTQK 315  
 QY 225 SLSLSPGK 232  
 Db 316 SISRSPGK 323  
 RESULT 11  
 I47160  
 Ig gamma 2b chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47160  
 R;Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A;Reference number: I47158; MUID:95015845; PMID:7930579  
 A;Accession: I47160  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 1-328 <KAC>  
 A;Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PFI  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>  
 F;133-202/Domain: immunoglobulin homology  
 Query Match 68.9%; Score 868.5; DB 2; Length 328;  
 Best Local Similarity 70.1%; Pred. No. 1.6e-58;  
 Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;  
 QY 11 CPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70  
 Db 106 CPICPACE -SPGPSVFIPFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
 QY 71 NVKTKPREQYNSTYRVSVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPRE 130  
 Db 165 TAQTRPKKEQFNSTYRVSVVLPVPIHQDWLNGKEFKCKVNNKDLPAPITRIISKAGQTRE 224  
 QY 131 PQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQ--PENNYKTTTPPVLSVGS 188  
 Db 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVWQRNGQPEPEGNVYRTTTPQQDVGDT 284  
 QY 189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSPGK 232  
 Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328  
 RESULT 13  
 I47162  
 Ig gamma 4 chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47162  
 R;Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A;Reference number: I47158; MUID:95015845; PMID:7930579  
 A;Accession: I47162  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 1-277 <KAC>  
 A;Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PFI  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 F;82-151/Domain: immunoglobulin homology <IMM>  
 Query Match 68.7%; Score 865; DB 2; Length 277;  
 Best Local Similarity 69.0%; Pred. No. 2.5e-58;  
 Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;  
 QY 8 THTCPCEP-APELLG-GPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65  
 Db 49 TKTTPCPICPACEGPGSAFIFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 108  
 QY 66 GVEVHNKTKPREQYNSTYRVSVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAK 125  
 Db 109 GVEVHTAQRPKKEQFNSTYRVSVVLPVPIHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 168  
 QY 126 VQPREPVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQ--PENNYKTTTPPV 183  
 Db 169 GQTRPEQVYTLPPPTPEELSRKSVITCLVIGFYPPDIDVWQRNGQPEPEGNVYRTTTP 228  
 QY 184 DSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSPGK 232  
 Db 229 DVDGTYFLYSKLAVDKASWQGGGIFQCAVMHEALHNHYTQKSIFKTPGK 277  
 RESULT 14  
 G2GP  
 Ig gamma-2 chain C region - guinea pig  
 C;Species: Cavia porcellus (guinea pig)  
 C;Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004

A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PFI  
 C;Genetics:  
 A;Gene: IgG2a  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 F;133-202/Domain: immunoglobulin homology <IMM>  
 Query Match 68.9%; Score 868.5; DB 2; Length 328;  
 Best Local Similarity 70.1%; Pred. No. 1.6e-58;  
 Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;  
 QY 11 CPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70  
 Db 106 CPICPACE -SPGPSVFIPFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
 QY 71 NVKTKPREQYNSTYRVSVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPRE 130  
 Db 165 TAQTRPKKEQFNSTYRVSVVLPVPIHQDWLNGKEFKCKVNNKDLPAPITRIISKAGQTRE 224  
 QY 131 PQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQ--PENNYKTTTPPVLSVGS 188  
 Db 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVWQRNGQPEPEGNVYRTTTPQQDVGDT 284  
 QY 189 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSPGK 232  
 Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328  
 RESULT 13  
 I47162  
 Ig gamma 4 chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47162  
 R;Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A;Reference number: I47158; MUID:95015845; PMID:7930579  
 A;Accession: I47162  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Molecule type: mRNA  
 A;Residues: 1-277 <KAC>  
 A;Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:g433129; PIDN:AAA52220.1; PFI  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 F;82-151/Domain: immunoglobulin homology <IMM>  
 Query Match 68.7%; Score 865; DB 2; Length 277;  
 Best Local Similarity 69.0%; Pred. No. 2.5e-58;  
 Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;  
 QY 8 THTCPCEP-APELLG-GPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65  
 Db 49 TKTTPCPICPACEGPGSAFIFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 108  
 QY 66 GVEVHNKTKPREQYNSTYRVSVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAK 125  
 Db 109 GVEVHTAQRPKKEQFNSTYRVSVVLPVPIHQDWLNGKEFKCKVNNKDLPAPITRIISKAK 168  
 QY 126 VQPREPVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVWESNGQ--PENNYKTTTPPV 183  
 Db 169 GQTRPEQVYTLPPPTPEELSRKSVITCLVIGFYPPDIDVWQRNGQPEPEGNVYRTTTP 228  
 QY 184 DSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQQRSLSPGK 232  
 Db 229 DVDGTYFLYSKLAVDKASWQGGGIFQCAVMHEALHNHYTQKSIFKTPGK 277  
 RESULT 14  
 G2GP  
 Ig gamma-2 chain C region - guinea pig  
 C;Species: Cavia porcellus (guinea pig)  
 C;Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004

C;Accession: A94553; A90352; A90359; A90384; A90385; A902151  
R;Trischmann, T.M.  
submitted to the Atlas, April 1975  
A;Reference number: A94553  
A;Accession: A94553  
A;Molecule type: protein  
A;Residues: 1-3 <TRI>  
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI0000017379E  
R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
A;Reference number: A90352; MUID:71058471; PMID:5538606  
A;Accession: A90352  
A;Molecule type: protein  
A;Residues: 4-68 <BIR>  
A;Cross-references: UNIPARC:UPI0000017379F  
R;Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am  
A;Reference number: A90359; MUID:71058486; PMID:5538616  
A;Accession: A90359  
A;Molecule type: protein  
A;Residues: 69-133;312-329 <TUR>  
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1  
R;Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A;Reference number: A90384; MUID:75036072; PMID:4429665  
A;Accession: A90384  
A;Molecule type: protein  
A;Residues: 134-226 <TRA>  
A;Cross-references: UNIPARC:UPI00001737A2  
R;Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A;Reference number: A90385; MUID:75036073; PMID:4609467  
A;Accession: A90385  
A;Molecule type: protein  
A;Residues: 227-311 <TR2>  
A;Cross-references: UNIPARC:UPI00001737A3  
R;Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A;Reference number: A90354; MUID:71058474; PMID:4922544  
A;Contents: annotation; disulfide bonds  
A;Note: Cys-16 is involved in a heavy-light chain bond  
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds  
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:21-81/Domain: immunoglobulin homology <IM1>  
F:135-204/Domain: immunoglobulin homology <IM2>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;  
Best Local Similarity 67.4%; Pred. No.1e-57; Mismatches 42; Indels 6; Gaps 2;  
Matches 157; Conservative 28;

Qy 1 EPKSCDKHTCPPEAPPELLGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 101 ZFBPC-----TCPKCPPENLGSPSVFIFPPKDTLMISLTPRVTCVVVDVSDPEVQF 156

Qy 61 NNYVDGVEVHVKTPREEQYNSTYRVSVLTCLVHQNMMNGKEYCKVSNKALPAPIEKT 120  
Db 157 TWFVDNKPVGNAETKPRVQYNTTFRVESVLPQHQDWLRGKFEKCKVYNKALPAPIEKT 216

Qy 121 ISKAKVQPREQYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT 178

Db 217 ISKTGAPRMPDVTTLPPSRDELSKSKSVTCLIIINFFPADIHVEWASNRVPVSEKEYKN 276  
Qy 179 TTPVLDVSGSFYLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSPG 231  
Db 277 TPPIEDAGSYFLYSKLTVDKSAWDGTVYTCVMHEALHNHYTQKAISRSPG 329

RESULT 15  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47158  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
A;Accession: I47158  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-328 <KAC>  
A;Cross-references: UNIPARC:UPI00000115523; EMBL:U03778; NID:9433121; PIDN:AA52216.1; P1  
C;Genetics:  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 67.3%; Score 847.5; DB 2; Length 328;  
Best Local Similarity 69.3%; Pred. No. 6.4e-57;  
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

Qy 10 TCPPEAPPELLGSPVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 69  
Db 105 TCPICPGCE-VAGSPSVFIFPPKDTLMISQTPVTCTVVDVSKHAELVQFSWYVDGVEV 163  
Qy 70 HNVKTKPREEQYNSTYRVSVLTCLVHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPR 129  
Db 164 HTAETRPKEQFNSTYRVSVLPQHQDWLRGKFEKCKVNNVDLPAPITRTISKAGQSR 223  
Qy 130 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDVSG 187  
Db 224 EPQVYTLPPPAEELSRSKVTLTCLVIGFYPPDIHVEWESNGQPEPTRTTPPQQDDVDG 283  
Qy 188 SFYLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSPG 232  
Db 284 TFFLYSKLAVDKARWDHGDGKFECAVMHEALHNHYTQKSISKTQCK 328

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Job time : 22.8551 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:43:39 ; Search time 127,768 Seconds  
(without alignment)  
1281.091 Million cell updates/sec

Title: US-09-847-208B-3  
Perfect score: 1260  
Sequence: 1 EPKSCDTHTCPCPAPELL.....MHEALHNYQORSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	IGHG1_HUMAN	P01857 homo sapien
2	1225	97.2	465	Q6GMX6_HUMAN	Q6gmx6 homo sapien
3	1225	97.2	466	Q6IN78_HUMAN	Q6in78 homo sapien
4	1225	97.2	469	Q569F4_HUMAN	Q569f4 homo sapien
5	1225	97.2	469	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
6	1225	97.2	470	Q7Z5W1_HUMAN	Q7z5w1 homo sapien
7	1225	97.2	470	Q6PJA4_HUMAN	Q6pja4 homo sapien
8	1225	97.2	472	Q6N089_HUMAN	Q6n089 homo sapien
9	1225	97.2	475	Q5EFES_HUMAN	Q5efes homo sapien
10	1225	97.2	475	Q6GMW7_HUMAN	Q6gmw7 homo sapien
11	1225	97.2	476	Q6GMX1_HUMAN	Q6gmx1 homo sapien
12	1225	97.2	679	Q6PQ08_HUMAN	Q6pq08 homo sapien
13	1221	96.9	473	Q6P055_HUMAN	Q6p055 homo sapien
14	1221	96.9	475	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
15	1221	96.9	480	Q6N094_HUMAN	Q6n094 homo sapien
16	1221	96.9	481	Q6N097_HUMAN	Q6n097 homo sapien
17	1221	96.9	482	Q7Z351_HUMAN	Q7z351 homo sapien
18	1219	96.7	348	Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1219	96.7	473	Q6MZV7_HUMAN	Q6mzv7 homo sapien
20	1219	96.7	478	Q6P181_HUMAN	Q6p181 homo sapien
21	1219	96.7	480	Q6PJF1_HUMAN	Q6pjf1 homo sapien
22	1218	96.7	466	Q6N096_HUMAN	Q6n096 homo sapien
23	1214	96.3	475	Q6N095_HUMAN	Q6n095 homo sapien
24	1214	96.3	544	Q6P195_HUMAN	Q6p195 homo sapien
25	1196	94.9	487	Q5ZL12_MOUSE	Q5zl12 mus sp. fr/
26	1164	92.4	475	Q5RE17_PONPY	Q5re17 pongo pygma
27	1138	90.3	354	Q86TT2_HUMAN	Q86tt2 homo sapien
28	1138	90.3	518	Q6N030_HUMAN	Q6n030 homo sapien
29	1138	90.3	519	Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1134	90.0	521	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
31	1128	89.5	290	IGHG3_HUMAN	P01860 homo sapien

32 1123 89.1 509 2 Q8NF17\_HUMAN Q8nf17 homo sapien  
33 1107 87.9 326 1 IGHG2\_HUMAN Ighg2 homo sapien  
34 1107 87.9 417 2 Q6N093\_HUMAN Q6n093 homo sapien  
35 1104 87.6 464 2 Q6MZU6\_HUMAN Q6mzu6 homo sapien  
36 1102 87.5 465 2 Q6P6C4\_HUMAN Q6p6c4 homo sapien  
37 1097 87.1 327 1 IGHG4\_HUMAN Ighg4 homo sapien  
38 1097 87.1 473 2 Q8TC63\_HUMAN Q8tc63 homo sapien  
39 1093 86.7 470 2 Q68CN4\_HUMAN Q68cn4 homo sapien  
40 1088 86.3 476 2 Q6MZK7\_HUMAN Q6mzk7 homo sapien  
41 883 70.1 323 1 GC\_RABIT P01870 oryctolagus  
42 877.5 69.6 337 2 Q95M34\_HORSE Q95m34 equus caball  
43 858 68.1 329 1 IGHG2\_CAVPO P01862 cavia porce  
44 813 64.5 333 1 GCB\_RAT P20761 rattus norv  
45 813 64.5 469 2 Q5M839\_RAT Q5m839 rattus norv

#### ALIGNMENTS

RESULT 1  
IGHG1\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN (2)  
RP PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN (3)  
RP PROTEIN SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN (4)  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).  
RN (5)  
RP PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN (6)  
RP DISULFIDE BONDS.

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RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds.";
RN Biochemistry 9:3188-3196(1970).
RP [7]
RX DISULFIDE BONDS.
RA MEDLINE=77070267; PubMed=1002129;
RX Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RA MEDLINE=81208100; PubMed=7236608;
RX Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
RN CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC GIM(3) marker and the GIM (non-1) markers.
CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR PIR; A93433; GHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1AQK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DSI; X-ray; H=1-101.
DR PDB; 1D6V; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1HZH; X-ray; H/K=1-330.
DR PDB; 1I72; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1OQX; X-ray; A/B=119-330.
DR PDB; 1T83; X-ray; A/B=107-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHG1.
DR MTM; 147100; ...
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
RN REGION 1 98 CH1.

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FT REGION 99 110 Hinge.
FT REGION 111 223 CH2.
FT REGION 224 330 CH3.
FT CARBOHYD 180 180 N-linked (GlcNAc...),
FT DISULFID 27 83 Interchain (with light chain).
FT DISULFID 103 103 Interchain (with heavy chain).
FT DISULFID 109 109 Interchain (with heavy chain).
FT DISULFID 112 112 Interchain (with heavy chain).
FT DISULFID 144 204 Interchain (with heavy chain).
FT DISULFID 250 308 Interchain (with heavy chain).
FT VARIANT 97 97 K -> R (in GIM(3) marker).
FT 239 /FTId=VAR_003886.
FT 239 D -> E (in GIM(non-1) marker).
FT /FTId=VAR_003887.
FT 241 L -> M (in GIM(non-1) marker).
FT /FTId=VAR_003888.
FT 1 NON_TER 1 1
FT STRAND 23 24
FT STRAND 26 33
FT STRAND 38 38
FT STRAND 41 41
FT TURN 42 45
FT TURN 48 49
FT STRAND 50 52
FT STRAND 57 58
FT TURN 59 61
FT STRAND 62 71
FT HELIX 73 75
FT TURN 76 78
FT STRAND 82 87
FT TURN 88 91
FT STRAND 92 97
FT TURN 102 103
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 149
FT STRAND 157 162
FT TURN 163 164
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FT STRAND 176 177
FT TURN 179 180
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FT HELIX 193 197
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FT STRAND 202 207
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FT STRAND 230 234
FT HELIX 238 242
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FT HELIX 297 301
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FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
Query Match 97.2%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 5.9e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 99 EPKSCDKTHTCPAPPELLGGPSVFLFPPPKOTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NYYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 159 NYYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOGPENNYKTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOGPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGVFSCSMHEALHNHYTQKSLSLSPGK 232
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGVFSCSMHEALHNHYTQKSLSLSPGK 330

RESULT 2
Q6GMX6 HUMAN
ID Q6GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Query Match 97.2%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 9.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPPKOTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 234 EPKSCDKTHTCPAPPELLGGPSVFLFPPPKOTLMISRTPEVTCVVVDVSHEDPEVKF 293
Qy 61 NYYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
Db 294 NYYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 353
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOGPENNYKTP 180
Db 354 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOGPENNYKTP 413
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGVFSCSMHEALHNHYTQKSLSLSPGK 232
Db 414 PVLDSGDSFFLYSKLTVDKSRWQQGVFSCSMHEALHNHYTQKSLSLSPGK 465

RESULT 3
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
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DR SMART; SM00409; IG: 2;
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0CBCEB81076E CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 9.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDEVK 60
DB 235 EPKSCDKHTHCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDEVK 294
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKCKVSNKALPAPIEKT 120
DB 295 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKCKVSNKALPAPIEKT 354
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
DB 355 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 414
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 232
DB 415 PVLDSGDSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 466

RESULT 4
Q569F4_HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
DR PROSITE; PS002518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
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Query Match          97.2%; Score 1225; DB 2; Length 469;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDEVK 60
DB 238 EPKSCDKHTHCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDDEVK 297
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKCKVSNKALPAPIEKT 120
DB 298 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKCKVSNKALPAPIEKT 357
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180
DB 358 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 417
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 232
DB 418 PVLDSGDSFFLYSKLTVDKSRWQOGNVFSCSVMHQALHNHYQOQSLSLSPGK 469
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RESULT 5
Q7Z7P5_HUMAN
ID Q7Z7P5_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -; mRNA.
DR HSSP; P01857; 1HZH.
DR SMR; Q7Z7P5; 20-469.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 3.
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DR SMART: SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5B812BAAF795C CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 469;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 238 EPKSCDKTHTCPPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
QY 61 NNYVDGVEVHNKTPPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 298 NNYVDGVEVHNKTPPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 357
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 358 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 417
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 418 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469

RESULT 6
Q725W1 HUMAN
ID Q725W1_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1.
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -; mRNA.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; I9_C1.
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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCPPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NNYVDGVEVHNKTPPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 299 NNYVDGVEVHNKTPPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 359 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
DB 419 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 7
Q6PJ4 HUMAN
ID Q6PJ4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJ4.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMK; Q6PUA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11ED7D99 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQWMMNGKEYCKVSNKALPAPIEKT 120
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQWMMNGKEYCKVSNKALPAPIEKT 358
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
DB 359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 418
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYQORSLSLSPGK 232
DB 419 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYQORSLSLSPGK 470

RESULT 8
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686p15220.
GN Name=DKF2p686p15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RC TISSUE=Rectum tumor;
RG The German CDNA Consortium;
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

us-09-847-208b-3.rup
Query Match 97.2%; Score 1225; DB 2; Length 472;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 241 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 300
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQWMMNGKEYCKVSNKALPAPIEKT 120
DB 301 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQWMMNGKEYCKVSNKALPAPIEKT 360
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
DB 361 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 420
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYQORSLSLSPGK 232
DB 421 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHAEALHNHYQORSLSLSPGK 472

RESULT 9
QSEFES HUMAN
ID QSEFES HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AAM82028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL. 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

us-09-847-208b-3.rup
Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQWMMNGKEYCKVSNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQWMMNGKEYCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
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364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 423
|||||
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPCK 232
|||||
Db 424 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPCK 475
|||||

RESULT 10
Q6GMW7 HUMAN PRELIMINARY; PRT; 475 AA.
ID Q6GMW7
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; Pf07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTCPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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Db 244 EPKSCDKHTCPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
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Qy 61 NWYVDGVEHNVKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
|||||
Db 304 NWYVDGVEHNVKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 363
|||||
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
|||||
Db 364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 423
|||||
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPCK 232
|||||
Db 424 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPCK 475
|||||

RESULT 11
Q6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
ID Q6GMX1
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; Pf07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 476;
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Best Local Similarity 97.0%; Pred. No. 9.3e-90;		Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
QY	1	EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	245	EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	304
QY	61	NWYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT	120
Db	305	NWYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT	364
QY	121	ISKAKVOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180
Db	365	ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	424
QY	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK	232
Db	425	PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKQSLSLSPGK	476
RESULT 12			
Q96PQ8 HUMAN			
ID	Q96PQ8	HUMAN PRELIMINARY; PRT; 679 AA.	
AC	Q96PQ8;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)	
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)	
DE	Factor VII active site mutant immunoconjugate.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;		
RA	Hu Z., Garen A.;		
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor		
RT	cells for immunotherapy in mouse models of prostatic cancer.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Hu Z., Garen A.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF272774; AAK58686.2; -, mRNA.		
DR	HSSP; P08709; 1KLI.		
DR	SMR; Q96PQ8; 39-180, 191-444, 447-679.		
DR	Ensembl; ENSG00000057593; Homo sapiens.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	GO; GO:0005093; F:calcium ion binding; IEA.		
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
DR	GO; GO:0004295; F:trypsin activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPRO00152; Asx_hydroxy1_S.		
DR	InterPro; IPRO00742; EGF 2.		
DR	InterPro; IPRO01881; EGF Ca.		
DR	InterPro; IPRO01438; EGF II.		
DR	InterPro; IPRO06209; EGF-like.		
DR	InterPro; IPRO02383; GLA_blood.		
DR	InterPro; IPRO07110; Ig-like.		
DR	InterPro; IPRO03597; Ig ci.		
DR	InterPro; IPRO03006; Ig MHC.		
DR	InterPro; IPRO01314; Peptidase_S1A.		
DR	InterPro; IPRO01254; Peptidase_S1_S6.		
DR	InterPro; IPRO00294; VitK_dep_GLA.		
DR	Pfam; PF07654; C1-set; 2.		
DR	Pfam; PF00008; EGF; 1.		
DR	Pfam; PF00594; Gla; 1.		
DR	Pfam; PF00089; Trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		
DR	PRINTS; PR00010; EGFBL00D.		
DR	PRINTS; PR00001; GLABLOOD.		
DR	SMART; SM00179; EGF_CA; 1.		

Query Match 97.2%; Score 1225; DB 2; Length 679;		Best Local Similarity 97.0%; Pred. No. 1.5e-89;		Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
QY	1	EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Db	448	EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	507		
QY	61	NWYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT	120		
Db	508	NWYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT	567		
QY	121	ISKAKVOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180		
Db	568	ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	627		
QY	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK	232		
Db	628	PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKQSLSLSPGK	679		
RESULT 13					
Q6P055 HUMAN					
ID	Q6P055	HUMAN PRELIMINARY; PRT; 473 AA.			
AC	Q6P055;				
DT	05-JUL-2004	(TrEMBLrel. 27, Created)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Periphereal Nervous System;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,				
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				

```
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Strausberg R.;  
RC TISSUE=Peripheral Nervous System;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC065820; AAH5820.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;  
  
Query Match 96.9%; Score 1221; DB 2; Length 473;  
Best Local Similarity 96.6%; Pred. No. 1.9e-89;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 242 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301  
  
QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKEYCKKVSNKALPAPIEKT 120  
DB 302 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKEYCKKVSNKALPAPIEKT 361  
  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 362 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 421  
  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK 232  
DB 422 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK 473  
  
RESULT 14  
Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.  
AC Q6MZQ6_  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686G11190.  
GN Name=DKFZp686G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640947; CAE45972.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D33AEC18 CRC64;  
  
Query Match 96.9%; Score 1221; DB 2; Length 480;  
Best Local Similarity 96.6%; Pred. No. 2e-89;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 242 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301  
  
QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKEYCKKVSNKALPAPIEKT 120  
DB 302 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKEYCKKVSNKALPAPIEKT 361  
  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 362 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 421  
  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK 232  
DB 422 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK 473  
  
RESULT 15  
Q6N094 HUMAN PRELIMINARY; PRT; 480 AA.  
AC Q6N094_  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE Hypothetical protein DKFZp686O01196.  
GN Name=DKFZp686O01196;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Esophagus tumor;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640622; CAE45776.1; -, mRNA.  
DR HSSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGC1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D33AEC18 CRC64;  
  
Query Match 96.9%; Score 1221; DB 2; Length 480;  
Best Local Similarity 96.6%; Pred. No. 2e-89;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 242 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301  
  
QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKEYCKKVSNKALPAPIEKT 120  
DB 302 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKEYCKKVSNKALPAPIEKT 361  
  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 362 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 421  
  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK 232  
DB 422 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK 473
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Db	309	NWYVDGVEVHNKTKPRREQYNSTYRVSVLT	VILHQNMMNGKEYCKKVS	NKALPAPIEKT 368
Qy	121	ISKAKQPREPQVYTLPPSRDELTKNOVSLT	CLVKGFYPSDIAVEWES	NGQPENNYKTTTP 180
Db	369	ISKAKQPREPQVYTLPPSRDELTKNOVSLT	CLVKGFYPSDIAVEWES	NGQPENNYKTTTP 428
Qy	181	PVLDSVGSFELYSKLTVDKSRWQQGNVFC	SCVMHEALHNNHYQQRS	LSLSPGK 232
Db	429	PVLDSVGSFELYSKLTVDKSRWQQGNVFC	SCVMHEALHNNHYQQRS	LSLSPGK 480

Search completed: November 30, 2005, 00:56:31  
Job time : 128.768 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:51:35 ; Search time 27.7391 Seconds  
(without alignments)  
691.469 Million cell updates/sec

Title: US-09-847-208B-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPPELL.....MHEALHNHYQORSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cgn2\_6/ptodata/1/iaa/5 COMB.pap.\*  
2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/PCRTUS COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	1	US-08-595-043A-50
2	1225	97.2	232	2	US-09-968-362A-26
3	1225	97.2	232	2	US-09-932-812A-26
4	1225	97.2	331	2	US-09-178-869-2
5	1225	97.2	331	2	US-09-761-413-2
6	1225	97.2	360	2	US-09-180-100-11
7	1225	97.2	360	2	US-09-949-713-11
8	1225	97.2	371	1	US-08-236-311-7
9	1225	97.2	371	2	US-08-457-918-7
10	1225	97.2	371	2	US-10-157-408-7
11	1225	97.2	376	2	US-09-180-100-22
12	1225	97.2	376	2	US-09-949-713-22
13	1225	97.2	379	2	US-10-679-999-9
14	1225	97.2	396	1	US-08-784-512-3
15	1225	97.2	396	2	US-09-176-228-3
16	1225	97.2	424	4	PCT-US95-03866-12
17	1225	97.2	424	4	PCT-US95-03866-14
18	1225	97.2	437	4	PCT-US96-10043-11
19	1225	97.2	442	4	US-08-472-888A-7
20	1225	97.2	442	4	PCT-US96-10043-9
21	1225	97.2	446	2	US-08-397-411-7
22	1225	97.2	449	1	US-08-458-516-13
23	1225	97.2	452	2	US-09-773-877B-16
24	1225	97.2	459	1	US-08-157-101A-7
25	1225	97.2	462	2	US-09-773-877B-18
26	1225	97.2	467	2	US-08-030-175-41
27	1225	97.2	467	2	US-08-030-175-42

28 1225 97.2 470 2 US-10-104-047-3730 Sequence 3730, Appl  
29 1225 97.2 475 2 US-09-740-002-27 Sequence 27, Appl  
30 1225 97.2 476 1 US-08-378-939-10 Sequence 10, Appl  
31 1225 97.2 476 2 US-08-487-550-4 Sequence 4, Appl  
32 1225 97.2 476 2 US-08-487-550-12 Sequence 12, Appl  
33 1225 97.2 476 2 US-09-526-098-4 Sequence 4, Appl  
34 1225 97.2 476 2 US-09-526-098-12 Sequence 12, Appl  
35 1225 97.2 476 2 US-09-383-916-4 Sequence 4, Appl  
36 1225 97.2 476 2 US-09-383-916-12 Sequence 12, Appl  
37 1225 97.2 476 2 US-09-758-173-4 Sequence 4, Appl  
38 1225 97.2 476 2 US-09-758-173-12 Sequence 12, Appl  
39 1225 97.2 476 2 US-09-576-424-4 Sequence 4, Appl  
40 1225 97.2 476 2 US-09-576-424-12 Sequence 12, Appl  
41 1225 97.2 478 2 US-08-487-550-8 Sequence 8, Appl  
42 1225 97.2 478 2 US-09-526-098-8 Sequence 8, Appl  
43 1225 97.2 478 2 US-09-383-916-8 Sequence 8, Appl  
44 1225 97.2 478 2 US-09-758-173-8 Sequence 8, Appl  
45 1225 97.2 478 2 US-09-576-424-8 Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-08-595-043A-50  
; Sequence 50, Application US/08595043A  
; Patent No. 5935824  
; GENERAL INFORMATION:  
; APPLICANT: SGARLATO, GREGORY D.  
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/595,043A  
; FILING DATE: 31-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: SGAR-00371  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-595-043A-50

Query Match 97.2%; Score 1225; DB 1; Length 232;

Best Local Similarity 97.0%; Pred. No. 3.5e-116;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Db 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

OY 61 NWYDGVGVHNVKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

Db 61 NWYDGVGVHNVKTKPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

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QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232

RESULT 2
US-09-968-362A-26
; Sequence 26, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; FILE REFERENCE: 03SUN2001
; CURRENT FILING DATE: 2001-10-01
; CURRENT APPLICATION NUMBER: US/09/968,362A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232

RESULT 3
US-09-932-812A-26
; Sequence 26, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; FILE REFERENCE: 02SUN2001
; CURRENT FILING DATE: 2001-08-17
; CURRENT APPLICATION NUMBER: US/09/932,812A
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-932-812A-26

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232

RESULT 4
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamman, Joseph P
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 100 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 160 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 219
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 220 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232
DB 280 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 331

RESULT 5
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
```

```
Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232
DB 181 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232

RESULT 4
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamman, Joseph P
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 100 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
DB 160 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 219
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 220 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 232
DB 280 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVMHGALHNHYOQRSLSLSPGK 331

RESULT 5
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
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; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/761,413
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/178,869
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-413-2

Query Match          97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 100 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
Qy 61 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 160 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 219
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 220 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 280 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 331

RESULT 6
US-09-180-100-11
; Sequence 11, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-11

Query Match          97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 129 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
Qy 61 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 189 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 248
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 280 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 331

RESULT 7
US-09-949-713-11
; Sequence 11, Application US/09949713
; Patent No. 6953847
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6953847io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-11

Query Match          97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 129 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
Qy 61 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 189 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 248
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 309 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 8
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311

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Qy 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 309 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 7
US-09-949-713-11
; Sequence 11, Application US/09949713
; Patent No. 6953847
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6953847io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/949,713
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US/09/180,100
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/JP97/01502
; PRIOR FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-713-11

Query Match          97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 129 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
Qy 61 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120
Db 189 NWYVDGVEVHNKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 248
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 309 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 8
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311

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/ FILING DATE: 02-MAY-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/936190
/ FILING DATE: 26-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/842777
/ FILING DATE: 18-FEB-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/250785
/ FILING DATE: 28-SEP-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/104329
/ FILING DATE: 02-OCT-1987
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hasak, Janet E.
/ REGISTRATION NUMBER: 28,616
/ REFERENCE/DOCKET NUMBER: 444P1C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1896
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 371 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-236-311-7

Query Match 97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
QY 61 NWTVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWTVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 319
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYTQKSLSLSPGK 232
Db 320 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYTQKSLSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918

/
/ FILING DATE: 02-MAY-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/936190
/ FILING DATE: 26-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/842777
/ FILING DATE: 18-FEB-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/250785
/ FILING DATE: 28-SEP-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/104329
/ FILING DATE: 02-OCT-1987
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hasak, Janet E.
/ REGISTRATION NUMBER: 28,616
/ REFERENCE/DOCKET NUMBER: 444P1C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1896
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 371 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-236-311-7

Query Match 97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
QY 61 NWTVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWTVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 319
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYTQKSLSLSPGK 232
Db 320 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYTQKSLSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918

/
/ FILING DATE: 1-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/236311
/ FILING DATE: 02-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/936190
/ FILING DATE: 26-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/842777
/ FILING DATE: 18-FEB-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/250785
/ FILING DATE: 28-SEP-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/104329
/ FILING DATE: 02-OCT-1987
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kubinec, Jeffrey S.
/ REGISTRATION NUMBER: 36,575
/ REFERENCE/DOCKET NUMBER: P0444P1C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-8228
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 371 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-457-918-7

Query Match 97.2%; Score 1225; DB 2; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
QY 61 NWTVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWTVDGVEVHNKTPRREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 319
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYTQKSLSLSPGK 232
Db 320 PVLDSGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYTQKSLSLSPGK 371

RESULT 10
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```



APPLICANT: Mann, Michael B.  
APPLICANT: Hecht, Randy I.  
TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Angen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/679,999  
FILING DATE: 06-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/568,528  
FILING DATE: 09-May-2000  
APPLICATION NUMBER: 09/267,517  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Knight, Matthew W.  
REGISTRATION NUMBER: 36,846  
REFERENCE/DOCKET NUMBER: A-416  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 379 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1  
OTHER INFORMATION: /note= "Met (ATG) starts at -1"  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-679-999-9

Query Match 97.2%; Score 1225; DB 2; Length 379;  
Best Local Similarity 97.0%; Pred. No. 7.1e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
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DB 2 EPKSCDKHTCCPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVWVDVSHEDPEVKF 61  
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 62 NWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 121  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 122 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 181  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYQORSLSLSPGK 232  
DB 182 PVLDSGDSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYQORSLSLSPGK 233

RESULT 14  
US-08-784-512-3  
Sequence 3, Application US/08784512  
Patent No. 5872209  
GENERAL INFORMATION:  
APPLICANT: BARTNIK, Eckart  
APPLICANT: EIDENMUELLER, Bernd  
APPLICANT: BUETTNER, Frank

APPLICANT: CATERSON, Bruce  
APPLICANT: HUGHES, Clare  
TITLE OF INVENTION: An artificial recombinant substrate (rAGS 1)  
TITLE OF INVENTION: and native aggregan to study the proteolytic activity of  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,512  
FILING DATE: 17-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 96100682.2  
FILING DATE: 18-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/311  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..396  
US-08-784-512-3

Query Match 97.2%; Score 1225; DB 1; Length 396;  
Best Local Similarity 97.0%; Pred. No. 7.6e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
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QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 225 NWYVDGVEVHNATKPREEQYNSTYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 284  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 285 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 344  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYQORSLSLSPGK 232  
DB 345 PVLDSGDSFPLYSKLTVDKSRWQOGNVFSCSVNMEALHNHYQORSLSLSPGK 396

RESULT 15  
US-09-176-228-3  
Sequence 3, Application US/09176228  
Patent No. 6180334  
GENERAL INFORMATION:  
APPLICANT: BARTNIK, Eckart  
APPLICANT: EIDENMUELLER, Bernd  
APPLICANT: BUETTNER, Frank  
APPLICANT: CATERSON, Bruce

APPLICANT: HUGHES, Clare  
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)  
TITLE OF INVENTION: and native aggregran to study the proteolytic activity of  
TITLE OF INVENTION: "Aggregranase" in cell culture systems  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/176,228  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,512  
FILING DATE: 17-JAN-1997  
APPLICATION NUMBER: EP 96100682.2  
FILING DATE: 18-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/311  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 396 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..396  
US-09-176-228-3

Query Match 97.2%; Score 1225; DB 2; Length 396;  
Best Local Similarity 97.0%; Pred. No. 7.6e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224  
Qy 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHONMMNGKEYKCKVSNKALPAPIEKT 120  
Db 225 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIEKT 284  
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
Db 285 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 344  
Qy 181 PVLDVGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232  
Db 345 PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 396

Search completed: November 30, 2005, 01:12:51  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2005, 00:56:45 ; Search time 97.087 Seconds  
(without alignments)  
998.449 Million cell updates/sec

Title: US-09-847-208B-3  
Perfect score: 1260  
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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1260	100.0	569	3	US-09-847-208-7
6	1260	100.0	569	4	US-10-000-439-7
7	1228	97.5	330	5	US-10-966-673-29
8	1225	97.2	232	3	US-09-996-357-10
9	1225	97.2	232	3	US-09-389-782-1
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11	1225	97.2	232	4	US-10-761-593A-26
12	1225	97.2	232	5	US-10-831-622-97
13	1225	97.2	232	5	US-10-800-497-26
14	1225	97.2	232	5	US-10-800-449-26
15	1225	97.2	232	5	US-10-964-215-97
16	1225	97.2	232	6	US-11-016-518A-26
17	1225	97.2	232	6	US-11-017-185-26
18	1225	97.2	234	5	US-10-627-556-684
19	1225	97.2	235	4	US-10-207-655-208
20	1225	97.2	235	5	US-10-627-556-2
21	1225	97.2	235	5	US-10-734-661A-6
22	1225	97.2	247	3	US-09-996-357-13
23	1225	97.2	251	4	US-10-008-063-18
24	1225	97.2	251	4	US-10-152-363A-6
25	1225	97.2	267	3	US-09-996-357-12
26	1225	97.2	269	5	US-10-609-783B-50
27	1225	97.2	285	6	US-11-018-102-11

28	1225	97.2	288	3	US-09-822-851B-14	Sequence 14, Appl
29	1225	97.2	288	4	US-10-119-637A-14	Sequence 14, Appl
30	1225	97.2	288	6	US-11-018-102-1	Sequence 1, Appl
31	1225	97.2	288	6	US-11-129-083-14	Sequence 14, Appl
32	1225	97.2	288	6	US-11-128-495-14	Sequence 14, Appl
33	1225	97.2	288	6	US-11-128-496-14	Sequence 14, Appl
34	1225	97.2	288	6	US-11-129-080-14	Sequence 14, Appl
35	1225	97.2	288	6	US-11-128-709-14	Sequence 14, Appl
36	1225	97.2	329	4	US-10-370-749-48	Sequence 48, Appl
37	1225	97.2	329	5	US-10-798-380-37	Sequence 37, Appl
38	1225	97.2	330	3	US-09-995-898A-15	Sequence 15, Appl
39	1225	97.2	330	3	US-09-892-549-38	Sequence 38, Appl
40	1225	97.2	330	4	US-10-047-542-20	Sequence 20, Appl
41	1225	97.2	330	4	US-10-269-805-68	Sequence 68, Appl
42	1225	97.2	330	4	US-10-310-719-8	Sequence 8, Appl
43	1225	97.2	330	4	US-10-112-582-1	Sequence 1, Appl
44	1225	97.2	330	4	US-10-320-231A-81	Sequence 81, Appl
45	1225	97.2	330	4	US-10-383-902A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-09-847-208-3  
; Sequence 3, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Daocheng  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
; FILE REFERENCE: UC67.002A  
; CURRENT APPLICATION NUMBER: US/09/847,208  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-208-3

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Matches	232;	Conservative	0;	Indels	0;
Gaps	0;				
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Qy	61	NWYDGVGVHVNKTKPREEQNSTYRVVSVTLVHQNMMNGKEYCKYKSNKALPAPIET	120		
Db	61	NWYDGVGVHVNKTKPREEQNSTYRVVSVTLVHQNMMNGKEYCKYKSNKALPAPIET	120		
Qy	121	ISKAKVQPREQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP	180		
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Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQQRSLSLSPGK	232		
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RESULT 2  
US-10-000-439-3  
; Sequence 3, Application US/10000439  
; Publication No. US20030064063A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

```

; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-3

Query Match      100.0%; Score 1260; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 120
DB 61 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232

RESULT 3
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match      100.0%; Score 1260; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 120
DB 159 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232

RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match      100.0%; Score 1260; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 120
DB 159 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 330

RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
US-09-847-208-7

Query Match      100.0%; Score 1260; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 330

RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match      100.0%; Score 1260; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 120
DB 159 NMYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIETK 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK 330

RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
US-09-847-208-7

Query Match      100.0%; Score 1260; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	EPKSCDKTHTCTCPCPAPPELLGSPSVFLPPPPKPKDTLMISRTPEVTCVVVDVSHEDDEVK	60
Db	1	EPKSCDKTHTCTCPCPAPPELLGSPSVFLPPPPKPKDTLMISRTPEVTCVVVDVSHEDDEVK	60
Qy	61	NWVDSGEVHNHVKTPREQYNSTYRVVSVLTVLIHQWMNGKEYCKVSKNALPAPIEKT	120
Db	61	NWVDSGEVHNHVKTPREQYNSTYRVVSVLTVLIHQWMNGKEYCKVSKNALPAPIEKT	120
Qy	121	ISKAKYQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTP	180
Db	121	ISKAKYQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTP	180
Qy	181	PVLDSVGSFPFLYSKLTVDKSRWQQGNVPCSCVMHEALHNHYQRSLSLSGK	232
Db	181	PVLDSVGSFPFLYSKLTVDKSRWQQGNVPCSCVMHEALHNHYQRSLSLSGK	232

```

RESULT 6
US-10-000-439-7
; Sequence 7, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRP
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IGE) sequence
US-10-000-439-7

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	Query Match	100.0%	Score 1260;	DB 4;	Length 569;
	Best Local Similarity	100.0%;	Prod. No. 3.2e-92;		
	Matches 232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Db	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Qy	61	NWYVDGVEVHNVKTKPREQYNSTRYVVSIVLTIVLHQNMMNGKEYCKVSNKALPAPIEKT	120		
Db	61	NWYVDGVEVHNVKTKPREQYNSTRYVVSIVLTIVLHQNMMNGKEYCKVSNKALPAPIEKT	120		
Qy	121	ISKAKVOPREPQVITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180		
Db	121	ISKAKVOPREPQVITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180		
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK	232		
Db	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK	232		

RESULT 7  
US-10-966-673-29  
; Sequence 29, Application US/10966673  
; Publication No. US20050226864A1  
; GENERAL INFORMATION:  
; APPLICANT: Protein Design Labs, Inc.  
; APPLICANT: Hinton, Paul R  
; APPLICANT: Tsurushita, Naoya  
; TITLE OF INVENTION: Altercation of Fc-Fusion Protein Serum Half-Lives By Mutagenesis  
; FILE REFERENCE: 05882.0039.NPUS07  
; CURRENT APPLICATION NUMBER: US/10/966,673

```

; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/562,627
; PRIOR FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US 60/511,687
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 330
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-10-966-673-29

```

	Query Match	97.5%	Score 1228;	DB 5;	Length 330;
	Best Local Similarity	97.4%;	Pred. No. 6.1e-90;		
	Matches 226;	Conservative	2;	Mismatches 4;	Indels 0; Gaps 0;
Qy	1	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Db	99	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	158		
Qy	61	NWYVDGVEVHNKTKPRREEYNSTYRVSVLTVTLHQNMNGKEYKKCVSKNALPAPIEKT	120		
Db	159	NWYVDGVEVHNKTKPRREEYNSTYRVSVLTVTLHQNMNGKEYKKCVSKNALPAPIEKT	218		
Qy	121	ISAKVQPREPQVYITLPPSRDELTKQVSLTCLVKGYPSDIAVEWESNGOPENNYKTP	180		
Db	219	ISAKGGPREPQVYITLPPSRDELTKQVSLTCLVKGYPSDIAVEWESNGOPENNYKTP	278		
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYQOQSLSLSPGK	332		
Db	279	PVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTKQSLSLSPGK	330		

RESULT 8  
 US-09-396-357-10  
 ; Sequence 10, Application US/09996357  
 ; Patent No. US20020133001A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gifter, Malcolm L  
 ; APPLICANT: Isreal, David I  
 ; APPLICANT: Joyal, John L  
 ; APPLICANT: Gosselin, Michael  
 ; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
 ; TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE

	Query Match	97.2%	Score 1225;	DB 3;	Length 232;
	Best Local Similarity	97.0%;	Pred. No. 7.1e-90;		
	Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	EPKSCDTHCTCPCPAPBELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVK	60		
Db	1	EPKSCDTHCTCPCPAPBELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVK	60		
Qy	61	NWYVDGVEVHNKTKPRREEQNSYRYVVSLTVLHQNMWCKEYCKVKSNKALPAPIEKT	120		
Db	61	NWYVDGVEVHNKTKPRREEQNSYRYVVSLTVLHQDNLNGKEYCKVKSNKALPAPIEKT	120		

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
DB 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYQORSLSLSPGK 232  
DB 181 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYTQKSLSLSPGK 232

RESULT 9

US-09-389-782-1  
; Sequence 1, Application US/09389782  
; Publication No. US20030144187A1  
; GENERAL INFORMATION:  
; APPLICANT: Wooden, Scott K.  
; APPLICANT: Mann, Michael B.  
; APPLICANT: Dunstan, Colin R.  
; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods  
; FILE REFERENCE: A-604  
; CURRENT APPLICATION NUMBER: US/09/389,782  
; CURRENT FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human  
US-09-389-782-1

Query Match 97.2%; Score 1225; DB 3; Length 232;  
Best Local Similarity 97.0%; Pred. No. 7.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNVKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
DB 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYQORSLSLSPGK 232  
DB 181 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYTQKSLSLSPGK 232

RESULT 10

US-10-617-619-7  
; Sequence 7, Application US/10617619  
; Publication No. US20040110929A1  
; GENERAL INFORMATION:  
; APPLICANT: Bjorn, Soren E  
; APPLICANT: Nicolaisen, Else M  
; APPLICANT: Jorgensen, Anker S  
; TITLE OF INVENTION: TF Binding Compound  
; FILE REFERENCE: 6455.200-US  
; CURRENT APPLICATION NUMBER: US/10/617,619  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/404,568  
; PRIOR FILING DATE: 2002-08-19  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Human

US-10-617-619-7

Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 7.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNVKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
DB 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYQORSLSLSPGK 232  
DB 181 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYTQKSLSLSPGK 232

RESULT 11

US-10-761-593A-26  
; Sequence 26, Application US/10761593A  
; Publication No. US20040175824A1  
; GENERAL INFORMATION:  
; APPLICANT: Sun, Lee-Hwei K  
; APPLICANT: Sun, Bill N  
; APPLICANT: Sun, Cecily R  
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological  
; TITLE OF INVENTION: activities  
; FILE REFERENCE: 02SUN2001-A  
; CURRENT APPLICATION NUMBER: US/10/761,593A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: 09/932812  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 26  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-761-593A-26

Query Match 97.2%; Score 1225; DB 4; Length 232;  
Best Local Similarity 97.0%; Pred. No. 7.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 1 EPKSCDKHTCCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
QY 61 NWYVDGVEVHNVKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 61 NWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
DB 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYQORSLSLSPGK 232  
DB 181 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCVMHEALHNNHYTQKSLSLSPGK 232

RESULT 12

US-10-831-622-97  
; Sequence 97, Application US/10831622  
; Publication No. US20040248257A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaye, Jonathan

APPLICANT: Wilkinson, Beverley  
TITLE OF INVENTION: SEQUENCE COMPOSITIONS AND METHODS OF USE

FILE REFERENCE: TSRI 810.1  
CURRENT APPLICATION NUMBER: US/10/831,622  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/467,206  
PRIOR FILING DATE: 2003-04-30

NUMBER OF SEQ ID NOS: 113  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 97

LENGTH: 232

TYPE: PRT

ORGANISM: Homo sapiens

US-10-831-622-97

Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 7.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

DB 1 EPKCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

DB 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

QY 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 232

DB 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 232

## RESULT 13

US-10-800-497-26

Sequence 26, Application US/10800497

Publication No. US20040259209A1

GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-

TITLE OF INVENTION: stimulating factor with

TITLE OF INVENTION: increased biological activities

FILE REFERENCE: 03SUN2001

CURRENT APPLICATION NUMBER: US/10/800,497

PRIOR FILING DATE: 2004-03-15

PRIOR APPLICATION NUMBER: US/09/968,362

PRIOR FILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 232

TYPE: PRT

ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains

US-10-800-497-26

Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 7.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

DB 1 EPKCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

DB 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

QY 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 232

DB 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 232

## RESULT 14

US-10-800-449-26

Sequence 26, Application US/10800449

Publication No. US20040265973A1

GENERAL INFORMATION:

APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill

APPLICANT: Sun, Cecily R

TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor

TITLE OF INVENTION: increased biological activities

FILE REFERENCE: 03SUN2001

CURRENT APPLICATION NUMBER: US/10/800,449

CURRENT FILING DATE: 2004-03-15

PRIOR APPLICATION NUMBER: US/09/968,362

PRIOR FILING DATE: 2001-10-01

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn version 3.1

SEQ ID NO 26

LENGTH: 232

TYPE: PRT

ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains

US-10-800-449-26

Query Match 97.2%; Score 1225; DB 5; Length 232;  
Best Local Similarity 97.0%; Pred. No. 7.1e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

DB 1 EPKCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

DB 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

DB 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180

QY 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 232

DB 181 PVLDSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 232

## RESULT 15

US-10-964-215-97

Sequence 97, Application US/10964215

Publication No. US20050152893A1

GENERAL INFORMATION:

APPLICANT: Kaye, Jonathan

TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION

TITLE OF INVENTION: OF TRANSPLANT REJECTION

FILE REFERENCE: TSRI 810.2

CURRENT APPLICATION NUMBER: US/10/964,215

CURRENT FILING DATE: 2004-10-12

PRIOR APPLICATION NUMBER: US 10/831,622

PRIOR FILING DATE: 2004-04-23

PRIOR APPLICATION NUMBER: US 60/467,206

PRIOR FILING DATE: 2003-04-30

NUMBER OF SEQ ID NOS: 113

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 97

LENGTH: 232

TYPE: PRT

ORGANISM: Homo sapiens

US-10-964-215-97

Query Match		97.2%	Score 1225;	DB 5;	Length 232;
Best Local Similarity		97.0%	Pred. No. 7.1e-90;		
Matches	225;	Conservative	3;	Mismatches	4;
				Indels	0;
				Gaps	0;
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Db	1	EPKSCDKTHTCPGPCAPELIGGPSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKF	60		
Qy	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQNMNGKEYCKVSNKALPAPIEKT	120		
Db	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQDNLNGKEYCKVSNKALPAPIEKT	120		
Qy	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP	180		
Db	121	ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP	180		
Qy	181	PVLDSVGSFELYSKLITVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	232		
Db	181	PVLDSGDSFELYSKLITVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	232		

Search completed: November 30, 2005, 01:16:48  
Job time : 98.087 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 30, 2005, 01:10:40 ; Search time 4.62319 Seconds  
(without alignments)  
152.100 Million cell updates/sec

Title: US-09-847-208B-3  
Perfect score: 1260  
Sequence: 1 EPKSCDKTHTCCPPAPPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/2/pubpaa/US10 NEW PUB.pap.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06 NEW PUB.pap.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07 NEW PUB.pap.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US08 NEW PUB.pap.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09 NEW PUB.pap.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCT NEW PUB.pap.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11 NEW PUB.pap.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60 NEW PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	330	7 US-11-022-289-11	Sequence 11, Appl
2	1225	97.2	444	7 US-11-172-320-6	Sequence 6, Appl
3	1225	97.2	452	7 US-11-016-503-6	Sequence 6, Appl
4	1225	97.2	459	1 US-10-949-720-390	Sequence 390, App
5	1225	97.2	462	7 US-11-016-503-8	Sequence 8, Appl
6	1225	97.2	551	7 US-11-022-289-7	Sequence 7, Appl
7	1225	97.2	551	7 US-11-022-289-8	Sequence 8, Appl
8	1225	97.2	557	7 US-11-016-503-4	Sequence 4, Appl
9	1225	97.2	557	7 US-11-022-289-4	Sequence 4, Appl
10	1225	97.2	557	7 US-11-022-289-5	Sequence 5, Appl
11	1225	97.2	557	7 US-11-022-289-6	Sequence 6, Appl
12	1225	97.2	567	7 US-11-016-503-2	Sequence 2, Appl
13	1225	97.2	567	7 US-11-016-503-10	Sequence 10, Appl
14	1225	97.2	771	1 US-10-949-720-389	Sequence 389, App
15	1220	96.8	489	1 US-10-835-475-11	Sequence 11, Appl
16	1220	96.8	514	1 US-10-835-475-2	Sequence 2, Appl
17	1219	96.7	330	7 US-11-022-289-1	Sequence 1, Appl
18	1219	96.7	548	7 US-11-022-289-3	Sequence 3, Appl
19	1219	96.7	557	7 US-11-022-289-2	Sequence 2, Appl
20	1219	96.7	564	7 US-11-022-289-10	Sequence 10, Appl
21	1219	96.7	579	7 US-11-174-186-41	Sequence 41, Appl
22	1198	95.1	531	7 US-11-008-727-18	Sequence 18, Appl
23	1195	94.8	455	7 US-11-016-503-14	Sequence 14, Appl
24	1195	94.8	458	7 US-11-016-503-12	Sequence 12, Appl
25	1195	94.8	458	7 US-11-016-503-16	Sequence 16, Appl

26	1189	94.4	227	7 US-11-008-727-14	Sequence 14, Appl
27	1176	93.3	430	7 US-11-016-503-17	Sequence 17, Appl
28	1107	87.9	326	7 US-11-144-248-28	Sequence 28, Appl
29	1107	87.9	470	7 US-11-144-248-45	Sequence 45, Appl
30	1107	87.9	470	7 US-11-144-248-46	Sequence 46, Appl
31	1107	87.9	470	7 US-11-144-248-49	Sequence 49, Appl
32	1107	87.9	473	7 US-11-144-248-50	Sequence 50, Appl
33	1104	87.6	450	7 US-11-025-712-12	Sequence 12, Appl
34	776	61.6	236	7 US-11-008-727-4	Sequence 4, Appl
35	776	61.6	470	7 US-11-008-727-20	Sequence 20, Appl
36	776	61.6	476	7 US-11-008-727-22	Sequence 22, Appl
37	776	61.6	509	7 US-11-008-727-16	Sequence 16, Appl
38	371.5	29.5	312	1 US-10-723-207-2	Sequence 2, Appl
39	333	26.4	325	1 US-10-723-207-1	Sequence 1, Appl
40	332.5	26.4	313	1 US-10-723-207-3	Sequence 3, Appl
41	330.5	26.2	313	1 US-10-723-207-4	Sequence 4, Appl
42	251	19.9	353	7 US-11-022-289-9	Sequence 9, Appl
43	241.5	19.2	236	7 US-11-022-289-12	Sequence 12, Appl
44	155	12.3	105	7 US-11-025-712-6	Sequence 6, Appl
45	151	12.0	230	1 US-10-894-730-371	Sequence 371, App

ALIGNMENTS

RESULT 1  
US-11-022-289-11  
; Sequence 11, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-022-289-11

Query Match 97.2%; Score 1225; DB 7; Length 330;  
Best Local Similarity 97.0%; Pred. No. 1e-98;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCCPPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 EPKSCDKTHTCCPPAPPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NWYDGVGEVHNKTPREEQYNSTYRVVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKT 120  
DB 159 NWYDGVGEVHNKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKT 218  
QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
DB 219 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 278  
QY 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 232  
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2  
US-11-172-320-6  
; Sequence 6, Application US/11172320  
; Publication No. US20050244413A1  
; GENERAL INFORMATION:  
; APPLICANT: Adolf, Guenther  
; APPLICANT: Baum, Anke

```
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-132-320-6

Query Match          97.2%; Score 1225; DB 7; Length 444;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 213 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 272

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 273 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 332

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 333 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 392

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 232
Db 393 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 444

RESULT 3
US-11-016-503-6
; Sequence 6, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-6

Query Match          97.2%; Score 1225; DB 7; Length 452;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-132-320-6

Query Match          97.2%; Score 1225; DB 7; Length 444;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 213 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 272

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 273 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 332

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 333 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 392

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 232
Db 393 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 444

RESULT 3
US-11-016-503-6
; Sequence 6, Application US/11016503
; Publication No. US20050245447A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016,503
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-016-503-6

Query Match          97.2%; Score 1225; DB 7; Length 452;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 221 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 280

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 281 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 340

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 341 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 400

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 232
Db 401 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 452

RESULT 4
US-10-949-720-390
; Sequence 390, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390

Query Match          97.2%; Score 1225; DB 1; Length 459;
Best Local Similarity 97.0%; Pred. No. 1.5e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 228 EPKSCDKTHTCCPPAPPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 287

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 288 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 347

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 407

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 232
Db 408 PVLDSGSGFFLYSKLTVDKSRWQOGNVFSCSVMHAEALHNHYTQKSLSLSPGK 459

RESULT 5
US-11-016-503-8
; Sequence 8, Application US/11016503
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Publication No. US20050245447A1
GENERAL INFORMATION:
APPLICANT: Nicholas J. Papadopoulos et al.
TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT APPLICATION NUMBER: US/11/016,503
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/009,852
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/138,133
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 462
TYPE: PRT
ORGANISM: Homo sapiens
US-11-016-503-8

Query Match          97.2%; Score 1225; DB 7; Length 462;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 231 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 290
QY 61 NWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 291 NWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 350
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
DB 351 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 410
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHNNHYTQKLSLSLSPGK 232
DB 411 PVLDSGSGFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHNNHYTQKLSLSLSPGK 462

RESULT 6
US-11-022-289-7
Sequence 7, Application US/11022289
Publication No. US20050249723A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
FILE REFERENCE: 185831/US/2
CURRENT APPLICATION NUMBER: US/11/022,289
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US 60/531,752
PRIOR FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 551
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic
US-11-022-289-7

Query Match          97.2%; Score 1225; DB 7; Length 551;
Best Local Similarity 97.0%; Pred. No. 1.9e-98;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
DB 219 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHNNHYTQKLSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVSCFVSWMHEALHNNHYTQKLSLSLSPGK 330

RESULT 8
US-11-016-503-4
Sequence 4, Application US/11016503
Publication No. US20050245447A1
GENERAL INFORMATION:
APPLICANT: Nicholas J. Papadopoulos et al.
TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT APPLICATION NUMBER: US/11/016,503
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/009,852
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
```



QY 61 NWYDGVVHNVKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 159 NWYDGVVHNAKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 218  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFFPSDIAVWESNGQPENNYKTTT 180  
DB 219 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFFPSDIAVWESNGQPENNYKTTT 278  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMSHEALHNHYQOQSLSLSPGK 232  
DB 279 PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVMSHEALHNHYQOQSLSLSPGK 330

RESULT 12  
US-11-016-503-2  
; Sequence 2, Application US/11016503  
; Publication No. US20050245447A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016,503  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-016-503-2

Query Match 97.2%; Score 1225; DB 7; Length 567;  
Best Local Similarity 97.0%; Pred. No. 1.9e-98;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 336 EPKSCDKHTHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 395  
QY 61 NWYDGVVHNVKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 396 NWYDGVVHNAKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 455  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFFPSDIAVWESNGQPENNYKTTT 180  
DB 456 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFFPSDIAVWESNGQPENNYKTTT 515  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMSHEALHNHYQOQSLSLSPGK 232  
DB 516 PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVMSHEALHNHYQOQSLSLSPGK 567

RESULT 13  
US-11-016-503-10  
; Sequence 10, Application US/11016503  
; Publication No. US20050245447A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016,503  
; CURRENT FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: US/10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-016-503-10

Query Match 97.2%; Score 1225; DB 7; Length 567;  
Best Local Similarity 97.0%; Pred. No. 1.9e-98;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 336 EPKSCDKHTHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 395  
QY 61 NWYDGVVHNVKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120  
DB 396 NWYDGVVHNAKTPREQYNSTYRVVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 455  
QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFFPSDIAVWESNGQPENNYKTTT 180  
DB 456 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFFPSDIAVWESNGQPENNYKTTT 515  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMSHEALHNHYQOQSLSLSPGK 232  
DB 516 PVLDSGDSFFLYSKLTVDKSRWQGNVFSQVMSHEALHNHYQOQSLSLSPGK 567

RESULT 14  
US-10-949-720-389  
; Sequence 389, Application US/10949720  
; Publication No. US20050249736A1  
; GENERAL INFORMATION:  
; APPLICANT: Kraenoprov, Valery  
; APPLICANT: Zozulya, Sergey  
; APPLICANT: Kertesz, Nathalie  
; APPLICANT: Reddy, Ramachandra  
; APPLICANT: Gill, Parkash  
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING  
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH  
; FILE REFERENCE: VASG-P02-002  
; CURRENT APPLICATION NUMBER: US/10/949,720  
; CURRENT FILING DATE: 2004-09-23  
; PRIOR APPLICATION NUMBER: US 60/454,432  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/454,300  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/800,350  
; PRIOR FILING DATE: 2004-03-12  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 389  
; LENGTH: 771  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Recombinant B4ECV3-FC protein  
US-10-949-720-389

Query Match 97.2%; Score 1225; DB 1; Length 771;  
Best Local Similarity 97.0%; Pred. No. 2.8e-98;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
DB 540 EPKSCDKHTHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 599

```
Qy 61 NWYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 600 NWYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 659
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 660 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 719
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232
Db 720 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 771
```

```
RESULT 15
US-10-835-475-11
; Sequence 11, Application US/10835475
; Publication No. US20050244410A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; TITLE OF INVENTION: Toll-Like Receptor Binding Agents and Uses Thereof
; FILE REFERENCE: CEN5022 USNP
; CURRENT APPLICATION NUMBER: US/10/835,475
; CURRENT FILING DATE: 2004-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Predicted Mature Form of TLR9 EC260-Fc Fusion
US-10-835-475-11
```

```
Query Match 96.8%; Score 1220; DB 1; Length 489;
Best Local Similarity 97.0%; Pred. No. 4.4e-98;
Matches 224; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 61
Db 238 PKSCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 297

Qy 62 WYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 121
Db 298 WYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 357

Qy 122 SKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 181
Db 358 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 417

Qy 182 VLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232
Db 418 VLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 468
```

Search completed: November 30, 2005, 01:17:04  
Job time : 5.62319 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2005, 00:34:13 ; Search time 152.464 Seconds  
(without alignment)  
922.194 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPPTVKILQSCDGGGHP.....HEAASPQTQORAVSVNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a  
-score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	100.0	320	AA019667	AA019667 Human IgE
2	1707	100.0	323	AAU80286	AAU80286 Human IgE
3	1707	100.0	323	AAU80285	AAU80285 Human IgE
4	1707	100.0	323	AAU80284	AAU80284 Human IgE
5	1707	100.0	324	AAR83559	AAR83559 Fc(epsilo
6	1707	100.0	325	AAR75225	AAR75225 Human IgE
7	1707	100.0	325	AAR77241	AAR77241 Human IgE
8	1707	100.0	327	ADY21849	ADY21849 Human IgE
9	1707	100.0	331	AAB03642	AAB03642 Human IgE
10	1707	100.0	331	ADD25768	ADD25768 Binding d
11	1707	100.0	331	ADY21799	ADY21799 Human IgE
12	1707	100.0	331	ADY21722	ADY21722 Human IgE
13	1707	100.0	367	AAP80291	AAP80291 Interleuk
14	1707	100.0	427	AA019666	AA019666 Human IgE
15	1707	100.0	428	AAU47863	AAU47863 Human Ig-
16	1707	100.0	428	AAU80283	AAU80283 Human IgE
17	1707	100.0	428	AAU50940	AAU50940 Human IgE
18	1707	100.0	428	AAE35113	AAE35113 Human imm
19	1707	100.0	428	ADD48440	ADD48440 Human pro
20	1707	100.0	428	ADY97382	ADY97382 Human IgE
21	1707	100.0	569	AA019668	AA019668 GE2 fusio
22	1707	100.0	574	ABG94250	ABG94250 Human IgE
23	1707	100.0	574	ABG80562	ABG80562 Human IgE
24	1707	100.0	574	ABP96592	ABP96592 Human IgE

25	1707	100.0	574	7	ADE97368	Ade97368 Human imm
26	1707	100.0	586	9	ADY22009	ADY22009 Antibody
27	1707	100.0	592	7	ADD25773	ADD25773 Binding d
28	1707	100.0	592	9	ADY21754	ADY21754 Antibody
29	1707	100.0	593	9	ADY21873	ADY21873 Antibody
30	1707	100.0	635	9	ADY21801	ADY21801 Antibody
31	1707	100.0	648	9	ADY21805	ADY21805 Antibody
32	1707	100.0	648	9	ADY21809	ADY21809 Antibody
33	1701	99.6	325	3	AAU79994	AAU79994 Human imm
34	1696	99.4	336	5	AAU80288	AAU80288 Human IgE
35	1696	99.4	441	5	AAU80287	AAU80287 Human var
36	1695.5	99.3	497	9	ADW24784	ADW24784 Human var
37	1695.5	99.3	497	9	ADW24742	ADW24742 Human var
38	1695.5	99.3	497	9	ADZ08809	ADZ08809 Mammalian
39	1695.5	99.3	497	9	ADZ08940	ADZ08940 Mammalian
40	1695.5	99.3	497	9	ADZ44466	ADZ44466 Human imm
41	1695.5	99.3	497	9	AEA16541	AEA16541 Human MCP
42	1695.5	99.3	497	9	ABE72776	ABE72776 Anti-Ltal
43	1693	99.2	493	1	AAP40065	AAP40065 Sequence
44	1685	98.7	325	2	AAR83582	AAR83582 CH2 to CH
45	1677	98.2	315	2	AAR85582	AAR85582 Fc(epsilo

## ALIGNMENTS

## RESULT 1

AA019667

ID AA019667 standard; protein; 320 AA.

XX

XX AA019667;

XX

XX 28-MAR-2003 (first entry)

XX

XX Human IgE heavy chain constant region CH2-CH3-CH4 portion.

XX Human; IgE; immunoglobulin E; immunotherapy; immune disease;

XX Fcepsilon receptor; autoimmune disease; constant region; heavy chain;

XX antiasthmatic; antiallergic; antiinflammatory; dermatological;

XX antiarthritic; antirheumatic; antidiabetic; neuroprotective;

XX CH2-CH3-CH4 region.

XX Homo sapiens.

XX

XX WO200288317-A2.

XX

XX 07-NOV-2002.

XX

XX 01-MAY-2002; 2002WO-US013527.

XX

XX 01-MAY-2001; 2001US-00847208.

XX

XX 24-OCT-2001; 2001US-00000439.

XX

XX (REGC ) UNIV CALIFORNIA.

XX

XX Saxon A, Zhang K, Zhu D;

XX

XX WPI; 2003-103456/09.

XX

XX New fusion molecules comprising polypeptide sequences that bind to IgG  
inhibitory receptor and native IgE receptor, useful for treating IgE-  
mediated hypersensitivity reactions, e.g. asthma or allergies, or  
autoimmune diseases.

XX

XX Claim 21; Fig 6; 116pp; English.

XX

XX The present invention relates to a fusion molecule comprising a first  
polypeptide sequence capable of specific binding to a native IgG  
inhibitory receptor consisting of an immune receptor tyrosine-based  
inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
functionally connected to a second polypeptide sequence capable of  
specific binding directly or indirectly to a native IgE receptor  
(FcepsilonR). Also provided are nucleotide sequences encoding such a

CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IGE-mediated biological response, preferably an IGE-mediated  
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
CC or symptoms resulting from, a type I hypersensitivity reaction in a  
CC subject receiving immunotherapy. The present sequence is the human IGE  
CC heavy chain constant region CH2-CH3-CH4 portion  
XX  
SQ Sequence 320 AA;

Query Match 100.0%; Score 1707; DB 6; Length 320;  
Best Local Similarity 100.0%; Pred. No. 4.1e-129; Mismatches 0; Gaps 0;  
Matches 320; Conservative 0; Indels 0; Gaps 0;  
QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60  
DB 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60  
QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120  
DB 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120  
QY 121 LFRKSPITITCLVVDLAPSKGTVNLWSRSGKPVNHSRKEEKORNGTLTVTSTLPVGT 180  
DB 121 LFRKSPITITCLVVDLAPSKGTVNLWSRSGKPVNHSRKEEKORNGTLTVTSTLPVGT 180  
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
DB 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
QY 241 NFWPDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLLEVTRAWEQKDEFICRAV 300  
DB 241 NFWPDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLLEVTRAWEQKDEFICRAV 300  
QY 301 HEAASPSQTVQRAVSNPGK 320  
DB 301 HEAASPSQTVQRAVSNPGK 320

RESULT 2  
AAU80286  
ID AAU80286 standard; protein; 323 AA.  
XX  
AC AAU80286;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Human IGE C2-C3-C4 domains for E.Coli expression.

XX IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
XX antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE;  
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
KW heavy chain C domain.

XX Homo sapiens.  
OS Synthetic.  
OS WO200220038-A2.  
XX  
XX 14-MAR-2002.  
XX  
XX 06-SEP-2001; 2001WO-DK000579.  
XX  
XX 06-SEP-2000; 2000DK-00001326.  
PR  
PR 15-SEP-2000; 2000US-0232831P.  
XX  
XX (PHAR-) PHARMEXA AS.  
XX  
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;  
PI  
XX WPI; 2002-383033/41.  
XX  
XX

DR N-PSDB; ABK511134.  
XX  
XX Inducing immune response against autologous immunoglobulin E in an  
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
PT epitope an/or B-cell epitope derived from the immunoglobulin.  
XX  
XX Disclosure; Page 112-113; 151pp; English.  
PS  
XX This invention relates to a novel method for inducing an immune response  
CC against autologous immunoglobulin E (IGE) in an animal. The method  
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell  
CC epitope (TH epitope) which is foreign to the animal, by antigen  
CC presenting cells (APCs) of the animal's immune system. The epitopes of  
CC the invention may be used as a vaccine against allergic diseases. The  
CC method of the invention is useful for inducing an immune response against  
CC autologous IGE in an animal, which is useful for downregulating  
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
CC asthma and atopic dermatitis. The present sequence represents the human  
CC IGE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli  
CC system, this sequence was used to create the epitopes of the invention  
XX  
SQ Sequence 323 AA;

Query Match 100.0%; Score 1707; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 4.2e-129; Mismatches 0; Gaps 0;  
Matches 320; Conservative 0; Indels 0; Gaps 0;  
QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60  
DB 4 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 63  
QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120  
DB 64 GELASTQSELTLSQKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 123  
QY 121 LFRKSPITITCLVVDLAPSKGTVNLWSRSGKPVNHSRKEEKORNGTLTVTSTLPVGT 180  
DB 124 LFRKSPITITCLVVDLAPSKGTVNLWSRSGKPVNHSRKEEKORNGTLTVTSTLPVGT 183  
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
DB 184 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243  
QY 241 NFWPDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLLEVTRAWEQKDEFICRAV 300  
DB 244 NFWPDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLLEVTRAWEQKDEFICRAV 303  
QY 301 HEAASPSQTVQRAVSNPGK 320  
DB 304 HEAASPSQTVQRAVSNPGK 323

RESULT 3  
AAU80285  
ID AAU80285 standard; protein; 323 AA.  
XX  
AC AAU80285;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
XX Human IGE C2-C3-C4 domains for mammalian expression.  
DE  
XX IGE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IGE;  
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
KW heavy chain C domain.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200220038-A2.  
PN

XX 14-MAR-2002.  
PD  
XX  
XX 06-SEP-2001; 2001WO-DK000579.  
PF  
XX  
XX 06-SEP-2000; 2000DK-00001326.  
PR  
XX  
XX 15-SEP-2000; 2000US-0232831P.  
PR  
XX  
XX (PHAR-) PHARMEXA AS.  
PA  
XX  
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;  
PI  
XX  
XX WPI; 2002-383033/41.  
DR  
XX  
XX N-PSDB; ABK51133.  
DR  
XX  
XX Inducing immune response against autologous immunoglobulin E in an  
PT  
XX animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
PT  
XX epitope an/or B-cell epitope derived from the immunoglobulin.  
PT  
XX  
XX Disclosure; Page 108-110; 151pp; English.  
PS  
XX  
XX This invention relates to a novel method for inducing an immune response  
CC  
XX against autologous immunoglobulin E (IgE) in an animal. The method  
CC  
XX comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
CC  
XX (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell  
CC  
XX epitope (TH epitope) which is foreign to the animal, by antigen  
CC  
XX presenting cells (APCs) of the animal's immune system. The epitopes of  
CC  
XX the invention may be used as a vaccine against allergic diseases. The  
CC  
XX method of the invention is useful for inducing an immune response against  
CC  
XX autologous IgE in an animal, which is useful for downregulating  
CC  
XX autologous IgE in the animal. This method is useful in the prevention and  
CC  
XX treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
CC  
XX asthma and atopic dermatitis. The present sequence represents the human  
CC  
XX IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian  
CC  
XX system, this sequence was used to create the epitopes of the invention  
XX  
XX Sequence 323 AA;  
SQ

Query Match 100.0%; Score 1707; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 4.2e-129;  
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FPPPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVDLSTASTTQE 60  
Db 4 FPPPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVDLSTASTTQE 63

Qy 61 GELASTQSELTLSQKHLSDRITYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRSPFD 120  
Db 64 GELASTQSELTLSQKHLSDRITYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRSPFD 123

Qy 121 LFIKSPPTITCLVVDLAPSKGTVNLTWSRASKPVNHSRKEKQNGTLTWTSTLPVGT 180  
Db 124 LFIKSPPTITCLVVDLAPSKGTVNLTWSRASKPVNHSRKEKQNGTLTWTSTLPVGT 183

Qy 161 RDWIGETVQCHVTPLPLALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
Db 184 RDWIGETVQCHVTPLPLALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVFSRLVTRAEWEQKDEFICRAV 300  
Db 244 NFMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVFSRLVTRAEWEQKDEFICRAV 303

Qy 301 HEAASPSQTVQRAVSNPKG 320  
Db 304 HEAASPSQTVQRAVSNPKG 323

RESULT 4  
AAU80284  
ID AAU80284 standard; protein; 323 AA.  
XX  
AC AAU80284;  
XX

DT 30-JUL-2002 (first entry)  
XX Human IgE heavy chain C2-C3-C4 domains.  
DE  
XX  
XX IgE; allergy; human; anti-allergic; immunosuppressive; antianaphylactic;  
KW antiasthmatic; dermatological; anti-inflammatory; immunoglobulin E; IgE;  
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
KW heavy chain C domain.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Domain 8..103  
FT /note= "IgE heavy chain C2 domain"  
FT 100..114  
FT Region /note= "Epitope including C2C3 linker"  
FT 104..111  
FT Region /note= "Linker between domains C2 and C3"  
FT 112..211  
FT Domain /label= "IgE heavy chain C3 domain"  
FT 139..145  
FT Region /note= "Epitope in BC loop"  
FT 167..175  
FT Region /note= "Epitope in DB loop"  
FT 196..206  
FT Domain /note= "Epitope in FG loop"  
FT 210..218  
FT Region /note= "Epitope including C3C4 linker"  
FT 212..215  
FT Region /note= "Linker between domains C3 and C4"  
FT 216..317  
FT Domain /note= "IgE heavy chain C4 domain"  
XX  
XX WO200220038-A2.  
XX  
XX 14-MAR-2002.  
XX  
XX 06-SEP-2001; 2001WO-DK000579.  
XX  
XX 06-SEP-2000; 2000DK-00001326.  
PR 15-SEP-2000; 2000US-0232831P.  
XX  
XX (PHAR-) PHARMEXA AS.  
PA  
XX  
XX Klysner S, Von Hoegen P, Voldborg B, Gautam A;  
PI  
XX  
XX WPI; 2002-383033/41.  
DR  
XX  
XX Inducing immune response against autologous immunoglobulin E in an  
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
PT epitope an/or B-cell epitope derived from the immunoglobulin.  
XX  
XX Disclosure; Page 105-106; 151pp; English.  
PS  
XX  
XX This invention relates to a novel method for inducing an immune response  
CC against autologous immunoglobulin E (IgE) in an animal. The method  
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell  
CC epitope (TH epitope) which is foreign to the animal, by antigen  
CC presenting cells (APCs) of the animal's immune system. The epitopes of  
CC the invention may be used as a vaccine against allergic diseases. The  
CC method of the invention is useful for inducing an immune response against  
CC autologous IgE in an animal, which is useful for downregulating  
CC autologous IgE in the animal. This method is useful in the prevention and  
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
CC asthma and atopic dermatitis. The present sequence represents the human  
CC IgE heavy chain C2-C3-C4 domains used to create the epitopes of the  
CC invention  
XX  
XX Sequence 323 AA;  
SQ

Query Match 100.0%; Score 1707; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 4.2e-129;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
Db	4 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 63
QY	61 GELASTQSELTLSQKHWSLDRYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db	64 GELASTQSELTLSQKHWSLDRYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 123
QY	121 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db	124 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 183
QY	181 RMIETGYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 240
Db	184 RMIETGYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 243
QY	241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLVTRAEWEQKDEFICRAV 300
Db	244 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLVTRAEWEQKDEFICRAV 303
QY	301 HEAASPQTQVRAVSNPGK 320
Db	304 HEAASPQTQVRAVSNPGK 323
RESULT 5	
AAR83559	
ID	AAR83559 standard; protein; 324 AA.
XX	
AC	AAR83559;
XX	
DT	06-MAR-1996 (first entry)
XX	
DE	Fc(epsilon) CH2'-CH4 protein sequence.
XX	
KW	Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
KW	constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
KW	histamine; anti-allergenic; vaccine; immune response.
XX	
OS	Synthetic.
XX	
PN	FR2715304-A1.
XX	
PD	28-JUL-1995.
XX	
PF	26-JAN-1994; 94FR-00000846.
XX	
PR	26-JAN-1994; 94FR-00000846.
XX	
PA	(INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
XX	
PI	Hurpin CM, Panero MJM;
XX	
XX	WPI; 1995-265243/35.
DR	N-PSDB; AAT01865.
XX	
PT	Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has
PT	epitope(s) not present in native IgE, also derived antibodies for
PT	treating or preventing allergies, inflammatory immune disease, etc.
XX	
FS	Claim 3; Page 32-33; 44pp; French.
XX	
CC	The amino acid sequence of the Fc(epsilon) CH2'-CH4 fragment covering
CC	amino acids 226-547. The DNA sequence was isolated from a human myeloma
CC	266BL cDNA library screened with a probe corresp. to the N-terminus of
CC	IgE. The region encoding amino acids 218-547 was cloned into the vector
CC	pWT211 under control of the tryptophan promoter. The resultant protein
CC	produced contains some non-Fc amino acids. These were removed by
CC	replacing their coding sequence with a bicistronic linker. The resultant
CC	construct encodes the Fc(epsilon) constant heavy region from amino acids
CC	226-547. When it is expressed in E.coli, the protein produced is a non-
CC glycosylated Fc(epsilon) fragment. Altering the pattern of glycosylation	
unmasks new antigenic sites thus rendering the Fc fragment immunogenic	
and able to induce antibodies that recognise native IgE but do not form	
histamine-releasing complexes. The Fc fragments can be used in anti-	
allergenic vaccines to modulate the intensity of immune responses	
mediated by IgE	
XX	
SQ	Sequence 324 AA;
Query Match 100.0%; Score 1707; DB 2; Length 324;	
Best Local Similarity 100.0%; Pred. No. 4.2e-129;	
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
Db	5 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 64
QY	61 GELASTQSELTLSQKHWSLDRYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db	65 GELASTQSELTLSQKHWSLDRYTCOVTYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 124
QY	121 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db	125 LFIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 184
QY	181 RMIETGYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 240
Db	185 RMIETGYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTLACLIQ 244
QY	241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLVTRAEWEQKDEFICRAV 300
Db	245 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLVTRAEWEQKDEFICRAV 304
QY	301 HEAASPQTQVRAVSNPGK 320
Db	305 HEAASPQTQVRAVSNPGK 324
RESULT 6	
AAR75225	
ID	AAR75225 standard; protein; 325 AA.
XX	
AC	AAR75225;
XX	
DT	25-MAR-2003 (revised)
DT	10-NOV-1995 (first entry)
XX	
DE	Human IgE Fc chain (amino acids 224-547) mutant sequence.
XX	
KW	IgE Fc fragment; antiallergic.
OS	Homo sapiens.
XX	
XX	
EH	Key Location/Qualifiers
FT	Misc-difference 1 /label= Val224
FT	/note= "any AA or deletion"
FT	Misc-difference 2 /label= Cys225
FT	/note= "Ala, any other AA, or deletion"
FT	Misc-difference 3 /label= Ser226
FT	/note= "any AA or deletion"
FT	Misc-difference 4 /label= Arg227
FT	/note= "any AA or deletion"
FT	Misc-difference 5 /label= Asp228
FT	/note= "any AA or deletion"
FT	Misc-difference 149 /label= Asn371
FT	/note= "glycosylation site"
FT	Misc-difference 172



```
FT /label= Aen394
FT /note= "glycosylation site"
FN W09514779-A1.
PD 01-JUN-1995.
PP 22-NOV-1994; 94WO-GB002561.
XX 22-NOV-1993; 93GB-00024013.
XX (THRE-) 3I RES EXPL LTD.
PA (CLLT ) CELLTech THERAPEUTICS LTD.
XX Gould HJ, Young RJ, Sutton BJ, Owens RJ;
XX WPI; 1995-206936/27.
DR N-PSDB; AAQ87474.
XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc - useful
FT to study and treat allergy.
XX Disclosure; Page 6; 55pp; English.
XX The sequence represents a mutant sequence of a human IgE-Fc chain (amino
CC acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or
CC Fc-epsilon FII IgE receptor sites on human cells. The protein is useful
CC in the study and treatment of allergy. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX Sequence 325 AA;
SQ
Query Match 100.0%; Score 1707; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.2e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTTQE 60
DB 6 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTTQE 65
QY 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHFTFEDSTKCCADSNPRGVSAVLSRPSFPD 120
DB 66 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHFTFEDSTKCCADSNPRGVSAVLSRPSFPD 125
QY 121 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGKPVNHSTRKEEKQKNGTLTVTSLPVG 180
DB 126 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGKPVNHSTRKEEKQKNGTLTVTSLPVG 185
QY 181 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
DB 186 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVETRAEWQKDEFICRAV 300
DB 246 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVETRAEWQKDEFICRAV 305
QY 301 HEAASPSQTVQRAVSVNPGK 320
DB 306 HEAASPSQTVQRAVSVNPGK 325
RESULT 7
ID AAR77241 standard; protein; 325 AA.
XX AAR77241;
XX 25-MAR-2003 (revised)
DT 10-NOV-1995 (first entry)
XX Human IgE Fc chain (amino acids 224-547) wild-type sequence.
XX IgE Fc fragment; antiallergic.
XX
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XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 149 /label= Aen371
FT /note= "glycosylation site"
FT Misc-difference 172 /label= Aen394
FT /note= "glycosylation site"
XX W09514779-A1.
FN PN
XX 01-JUN-1995.
XX 22-NOV-1994; 94WO-GB002561.
XX 22-NOV-1993; 93GB-00024013.
XX (THRE-) 3I RES EXPL LTD.
PA (CLLT ) CELLTech THERAPEUTICS LTD.
XX Gould HJ, Young RJ, Sutton BJ, Owens RJ;
XX WPI; 1995-206936/27.
DR N-PSDB; AAQ91170.
XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc - useful
FT to study and treat allergy.
XX Disclosure; Page 35-36; 55pp; English.
XX The sequence represents the wild-type sequence of a human IgE-Fc chain
CC (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI
CC and/or Fc-epsilon FII IgE receptor sites on human cells. The sequence is
CC preferably mutated (see AAR75225) to represent a protein encoding a
CC protein where Cys225 is mutated, optionally together with Val224, Ser226
CC and Arg227. The protein is useful in the study and treatment of allergy.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 325 AA;
SQ
Query Match 100.0%; Score 1707; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.2e-129;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTTQE 60
DB 6 FTPPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTASTTQE 65
QY 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHFTFEDSTKCCADSNPRGVSAVLSRPSFPD 120
DB 66 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHFTFEDSTKCCADSNPRGVSAVLSRPSFPD 125
QY 121 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGKPVNHSTRKEEKQKNGTLTVTSLPVG 180
DB 126 LFIRKSPITICLVVDLAPSKGTVNLTSRASKGKPVNHSTRKEEKQKNGTLTVTSLPVG 185
QY 181 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
DB 186 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVETRAEWQKDEFICRAV 300
DB 246 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVETRAEWQKDEFICRAV 305
QY 301 HEAASPSQTVQRAVSVNPGK 320
DB 306 HEAASPSQTVQRAVSVNPGK 325
RESULT 8
ADY21849
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ADY21849 standard; protein; 327 AA.  
 ADY21849;  
 05-MAY-2005 (first entry)  
 Human IgE CH2-CH3-CH4 region.  
 Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;  
 antibody engineering; cancer; neoplasm; cytostatic; immune disorder;  
 graves disease; antithyroid; endocrine disease; hashimoto's disease;  
 immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;  
 inflammation; musculoskeletal disease; systemic lupus erythematosus;  
 antiinflammatory; dermatological; dermatological disease;  
 metabolic disorder; sjogrens syndrome; ocular disease;  
 thrombocytopenic purpura; hemostatic; hematological disease;  
 multiple sclerosis; neuroprotective; neurological disease;  
 myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;  
 fungicide; viral infection; virucide; parasitic infection; antiparasitic;  
 fusion protein.  
 Homo sapiens.  
 WO2005017148-A1.  
 24-FEB-2005.  
 24-DEC-2003; 2003WO-US041600.  
 26-JUL-2003; 2003US-00627556.  
 (TRUB-) TRUBION PHARM INC.  
 Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
 WPI; 2005-182370/19.  
 N-PSDB; ADY21848.  
 New non-naturally occurring single chain protein comprising polypeptides  
 with binding domain, connecting regions and N-terminally truncated  
 immunoglobulin, having immunological activity, useful for neutralizing  
 infectious agent.  
 Disclosure; Page 365; 590pp; English.  
 The invention relates to a non-naturally occurring single chain protein  
 (1) comprising a first polypeptide having a binding domain polypeptide  
 capable of binding to a target molecule, the binding domain polypeptide  
 comprising a heavy chain variable region, which comprises an amino acid  
 substitution or deletion at one or more amino acid residues, a second  
 polypeptide comprising a connecting region attached to the first  
 polypeptide, and a third polypeptide comprising an N-terminally truncated  
 immunoglobulin heavy chain constant region polypeptide attached to the  
 second polypeptide, where the non-naturally occurring single-chain  
 protein is capable of an immunological activity. Also included are  
 reducing a target cell population in a subject (involving administering  
 to the subject a protein that is less than 150 kD, which involves  
 treating the target cell population with a first protein or peptide that  
 binds to cells within the target cell population, and treating the target  
 cell population with a second protein or peptide that capable of at least  
 one of binding an Fc receptor, inducing target cell apoptosis, or fix  
 complements, where the first protein or peptide molecule is directly  
 connected to the second protein or peptide molecule or, optionally, the  
 first protein or peptide molecule and the second protein or peptide  
 molecule are linked by a third protein or peptide molecule, and where the  
 protein molecule is not an antibody, a member of the TNF family or the  
 TNF receptor family, and is not conjugated with a bacterial toxin, a  
 cytotoxic drug, or a radioisotope), depleting cells in an animal  
 (involving administering a modified IGE protein into the blood stream of  
 an animal), a polynucleotide that encodes the polypeptide of the  
 invention, a cell containing the polynucleotide, a recombinant vector  
 capable of expressing the polypeptide, expressing the polypeptide, a  
 composition comprising the polypeptide) in combination with one or more

CC additional therapeutic compounds, displaying recombinant molecules (which  
 CC molecules include a native or engineered immunoglobulin heavy chain  
 CC variable region, the improvement comprising an immunoglobulin heavy chain  
 CC region that includes one or more mutation, substitution, alteration,  
 CC and/or deletion at one or more amino acid residue corresponding to  
 CC positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable  
 CC region) and a non-naturally occurring single chain antigen-binding  
 CC protein comprising protein having a mutation chosen from a list given in  
 CC the specification. The polypeptides of the invention comprise single  
 CC chain antibodies (scFv, with or without mutated residues) linked via an  
 CC immunoglobulin hinge region (wild-type or mutants where the cysteines are  
 CC changed to serines/prolines and denoted (SSS-P/H, (CSC-S)H etc) to an  
 CC immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which  
 CC may also have mutations in CH2 (e.g. F256N) or a truncated CH3 (e.g. F4  
 CC CH3, a 4 amino acid deletion). The polypeptide may be further linked to a  
 CC non-antibody protein such as the transmembrane and cytoplasmic tail  
 CC (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are  
 CC useful for neutralization of an infectious agent (where the infectious  
 CC agent is a bacterium, a virus, a parasite, or a fungus) and also for  
 CC treatment of cancer, immune disorders, Grave's disease, Hashimoto's  
 CC disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's  
 CC syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia  
 CC gravis. The present sequence is an antibody peptide or fragment (scFv,  
 CC hinge, CH region, VL or VH) used in a fusion protein of the invention.  
 CC  
 SQ Sequence 327 AA;  
 Query Match 100.0%; Score 1707; DB 9; Length 327;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-129;  
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FTPTVKILQSSCDGGCHPPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60  
 DB 8 FTPTVKILQSSCDGGCHPPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 67  
 QY 61 GELASTQSELTLSQKHWSLDRTYTCVITYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 120  
 DB 68 GELASTQSELTLSQKHWSLDRTYTCVITYQGHFTFEDSTKKCADSNPRGVSAYLSRSPFD 127  
 QY 121 LFIKSPITITCLVVDLAPSKGTNLTWRSASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180  
 DB 128 LFIKSPITITCLVVDLAPSKGTNLTWRSASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 187  
 QY 181 RWIEGETYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
 DB 188 RWIEGETYQCRVTHPHLPALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247  
 QY 241 NMPEDISVQWLHNEVQLPDARHSTTPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300  
 DB 248 NMPEDISVQWLHNEVQLPDARHSTTPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 307  
 QY 301 HEAASPSQTVQRAVSNPGK 320  
 DB 308 HEAASPSQTVQRAVSNPGK 327  
 RESULT 9  
 AAB03642  
 ID AAB03642 standard; protein; 331 AA.  
 AC AAB03642;  
 XX  
 XX 22-NOV-2000 (first entry)  
 XX Human IgE heavy chain constant regions 2, 3 and 4.  
 DE Human IgE heavy chain constant regions 2, 3 and 4.  
 KW Human; immunoglobulin E; IgE, vaccination; infection; allergy; asthma;  
 KW eczema; immunogenic peptide.  
 OS Homo sapiens.  
 XX  
 PN WO200025722-A2.  
 XX

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PD 11-MAY-2000.
XX
XX 21-OCT-1999; 99WO-SE001896.
XX
XX 02-NOV-1998; 98US-0106652P.
XX 22-SEP-1999; 99US-00401636.
XX
XX (RESI-) RESISTENTIA PHARM AB.
XX
XX Hellman LT;
XX
XX WPI; 2000-365342/31.
XX
XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.
XX
XX Disclosure; Fig 1; 50pp; English.
XX
XX The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2, 3 and 4 of the human IgE. It was used to
XX construct a number of immunogenic peptides which consisted of regions of
XX IgE from different mammals, which appear to cause a stronger polyclonal
XX anti-self IgE response than peptides consisting of the same regions from
XX one mammal. Immunogenic peptides, particularly those consisting of
XX different heavy chain constant regions, can be used for vaccination in
XX humans, against bacterial and viral infections and allergies, such as
XX asthma, fur, pollen and food allergies and eczema
XX
XX Sequence 331 AA;
XX
XX Query Match 100.0%; Score 1707; DB 3; Length 331;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-129; Mismatches 0; Indels 0; Gaps 0;
XX Matches 320; Conservative 0;
XX
QY 1 FTPTVKILQSCDCGGHFPPTIQLLCVSGYTPGTINITWLEDQVMDVDLSTASTTQEE 60
DB 12 FTPTVKILQSCDCGGHFPPTIQLLCVSGYTPGTINITWLEDQVMDVDLSTASTTQEE 71
QY 61 GELASTQSELTLSQKHWSLSDRTYTCQVYTGHTFEDSTKCCADSNPRGVSAYLSRPSFPD 120
DB 72 GELASTQSELTLSQKHWSLSDRTYTCQVYTGHTFEDSTKCCADSNPRGVSAYLSRPSFPD 131
QY 121 LFIKSPITCLVLDLAPSKGVNLTWSRASKPVNHSRKEKQKORNGTLTSTLPGVT 180
DB 132 LFIKSPITCLVLDLAPSKGVNLTWSRASKPVNHSRKEKQKORNGTLTSTLPGVT 191
QY 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPWPGRDKRTIACLIQ 240
DB 192 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPWPGRDKRTIACLIQ 251
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGFFVFSRLEVTRAEWQKDEPICRAV 300
DB 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGFFVFSRLEVTRAEWQKDEPICRAV 311
QY 301 HEAASPSQTVQRAVSNPCK 320
DB 312 HEAASPSQTVQRAVSNPCK 331
XX
XX RESULT 10
XX ADD25768 standard; protein; 331 AA.
XX
XX AC ADD25768;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE Binding domain-immunoglobulin fusion protein-associated protein #152.
XX
XX Binding domain; immunoglobulin; fusion protein; cytostatic;
XX KW antithyroid; immunosuppressive; antidiabetic; antithyroid;
XX KW neuroprotective; hinge region; immunoglobulin heavy chain;
XX CH2 constant region; CH3 constant region; IgG1;
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KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
XX type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
XX Unidentified.
XX
XX US2003118592-A1.
XX
XX 26-JUN-2003.
XX
XX 25-JUL-2002; 2002US-00207655.
XX
XX 17-JAN-2001; 2001US-0367358P.
XX 17-JAN-2002; 2002US-00053530.
XX 03-JUN-2002; 2002US-0385631P.
XX
XX (GENE-) GENE-CRAFT INC.
XX
XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
XX WPI; 2003-801317/75.
XX
XX New binding domain-immunoglobulin fusion protein, useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 329; 157pp; English.
XX
XX The invention relates to a binding domain-immunoglobulin fusion protein
XX comprising a binding domain polypeptide that is fused to an
XX immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CH2 constant region polypeptide that is fused to the hinge region
XX polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX polypeptide that is fused to the CH2 constant region polypeptide. The
XX hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
XX hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
XX region polypeptide derived from (a) having 3 or more cysteine residues;
XX where the mutated human IgG1 immunoglobulin hinge region polypeptide
XX contains 2 cysteine residues, where the first cysteine is not mutated; a
XX mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
XX (a) having 3 or more cysteine residues, where the mutated human IgG1
XX immunoglobulin hinge region polypeptide contains no more than one
XX cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
XX polypeptide, derived from (a) having 3 or more cysteine residues; where
XX the mutated human IgG1 immunoglobulin hinge region polypeptide contains
XX no cysteine residues. The binding domain-immunoglobulin fusion protein is
XX capable of at least one immunological activity comprising fixation. The
XX dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
XX binding domain polypeptide is capable of specifically binding to an
XX antigen. Also included are an isolated polynucleotide encoding the
XX binding domain-immunoglobulin fusion protein, a recombinant expression
XX construct comprising the polynucleotide (operably linked to a promoter),
XX a host cell transformed or transfected with a recombinant expression
XX construct, producing the binding domain-immunoglobulin fusion protein, a
XX pharmaceutical composition comprising the binding domain-immunoglobulin
XX fusion protein or polynucleotide and a carrier, and treating a subject
XX having or suspected of having a malignant condition or a B-cell disorder.
XX The binding domain-immunoglobulin fusion protein is useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
XX myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
XX sclerosis or autoimmune disease. The present sequence is a binding domain
XX -immunoglobulin fusion protein-associated protein sequence. Note: The
XX sequence data for this patent formed part of the printed specification
XX and is also available in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
XX identified the sequences in the printed specification by their SEQ ID
XX number therefore none of the sequences can be explicitly identified.
XX
XX Sequence 331 AA;
XX
XX Query Match 100.0%; Score 1707; DB 7; Length 331;
```

Best Local Similarity 100.0%; Pred. No. 4.3e-129; Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PS	Disclosure; Page 352; 590pp; English.
QY	1 FTFPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60	CC	The invention relates to a non-naturally occurring single chain protein (I) comprising a first polypeptide having a binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide comprising a heavy chain variable region, which comprises an amino acid substitution or deletion at one or more amino acid residues, a second polypeptide comprising a connecting region attached to the first polypeptide, and a third polypeptide comprising an N-terminally truncated immunoglobulin heavy chain constant region polypeptide attached to the second polypeptide, where the non-naturally occurring single-chain protein is capable of an immunological activity. Also included are reducing a target cell population in a subject (involving administering to the subject a protein that is less than 150 kD, which involves treating the target cell population with a first protein or peptide that binds to cells within the target cell population, and treating the target cell population with a second protein or peptide that capable of at least one of binding an Fc receptor, inducing target cell apoptosis, or fix complements, where the first protein or peptide molecule is directly connected to the second protein or peptide molecule or, optionally, the first protein or peptide molecule and the second protein or peptide molecule are linked by a third protein or peptide molecule, and where the protein molecule is not an antibody, a member of the TNF family or the TNF receptor family, and is not conjugated with a bacterial toxin, a cytotoxic drug, or a radioisotope), depleting cells in an animal (involving administering a modified IgE protein into the blood stream of an animal), a polynucleotide that encodes the polypeptide of the invention, a cell containing the polynucleotide, a recombinant vector capable of expressing the polypeptide, expressing the polypeptide, a composition comprising the polypeptide) in combination with one or more additional therapeutic compounds, displaying recombinant molecules (which molecules include a native or engineered immunoglobulin heavy chain variable region, the improvement comprising an immunoglobulin heavy chain region that includes one or more mutation, substitution, alteration, and/or deletion at one or more amino acid residue corresponding to positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable region) and a non-naturally occurring single chain antigen-binding protein comprising protein having a mutation chosen from a list given in the specification. The polypeptides of the invention comprise single chain antibodies (scFv, with or without mutated residues) linked via an immunoglobulin hinge region (wild-type or mutants where the cysteines are changed to serines/prolines and denoted (SSS-P)H, (CSC-S)H etc) to an immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which may also have mutations in CH2 (e.g. T258N) or a truncated CH3 (e.g. T4 CH3, a 4 amino acid deletion). The polypeptide may be further linked to a non-antibody protein such as the transmembrane and cytoplasmic tail (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are useful for neutralization of an infectious agent (where the infectious agent is a bacterium, a virus, a parasite, or a fungus) and also for treatment of cancer, immune disorders, Grave's disease, Hashimoto's disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia gravis. The present sequence is an antibody peptide or fragment (scFv, hinge, CH region, VL or VH) used in a fusion protein of the invention.
QY	61 GELASTQSELTLSQKHWSLDRITYTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120	QY	61 GELASTQSELTLSQKHWSLDRITYTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120
DB	8 FTFPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 67	DB	8 FTFPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 67
QY	121 LFRKSPPTITCLVLDLAPSKGTVNLTWASRSGKPVNHSRKEKQNGTLTWTSTLTPVGT 180	QY	61 GELASTQSELTLSQKHWSLDRITYTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120
DB	128 LFRKSPPTITCLVLDLAPSKGTVNLTWASRSGKPVNHSRKEKQNGTLTWTSTLTPVGT 187	DB	68 GELASTQSELTLSQKHWSLDRITYTCQVITYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 127
QY	181 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLAQLIQ 240	QY	121 LFRKSPPTITCLVLDLAPSKGTVNLTWASRSGKPVNHSRKEKQNGTLTWTSTLTPVGT 180
DB	188 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLAQLIQ 247	DB	128 LFRKSPPTITCLVLDLAPSKGTVNLTWASRSGKPVNHSRKEKQNGTLTWTSTLTPVGT 187
QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300	QY	181 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLAQLIQ 240
DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307	DB	188 RDWIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLAQLIQ 247
QY	301 HEAASPSQTVQRAVSNPGK 320	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
DB	308 HEAASPSQTVQRAVSNPGK 327	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
RESULT 11		QY	301 HEAASPSQTVQRAVSNPGK 320
ADY21799		DB	308 HEAASPSQTVQRAVSNPGK 327
ID	ADY21799 standard; protein; 331 AA.	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
AC	ADY21799;	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
DT	05-MAY-2005 (first entry)	QY	301 HEAASPSQTVQRAVSNPGK 320
XX	Human IgE Fc (CH2-CH3-CH4) protein.	DB	308 HEAASPSQTVQRAVSNPGK 327
DE	Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
KW	antibody engineering; cancer; neoplasm; cytostatic; immune disorder;	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
KW	graves disease; antithyroid; endocrine disease; hashimoto's disease;	QY	301 HEAASPSQTVQRAVSNPGK 320
KW	immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;	DB	308 HEAASPSQTVQRAVSNPGK 327
KW	inflammation; musculoskeletal disease; systemic lupus erythematosus;	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
KW	antiinflammatory; dermatological; dermatological disease;	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
KW	metabolic disorder; sjogrens syndrome; ocular disease;	QY	301 HEAASPSQTVQRAVSNPGK 320
KW	thrombocytopenic purpura; hemostatic; hematological disease;	DB	308 HEAASPSQTVQRAVSNPGK 327
KW	multiple sclerosis; neuroprotective; neurological disease;	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
KW	myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
KW	fungicide; viral infection; virucide; parasitic infection; antiparasitic;	QY	301 HEAASPSQTVQRAVSNPGK 320
XX	fusion protein.	DB	308 HEAASPSQTVQRAVSNPGK 327
OS	Homo sapiens.	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
XX	WO2005017148-A1.	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
PN	24-FEB-2005.	QY	301 HEAASPSQTVQRAVSNPGK 320
XX	24-DEC-2003; 2003WO-US041600.	DB	308 HEAASPSQTVQRAVSNPGK 327
XX	26-JUL-2003; 2003US-00627556.	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
PR	(TRUB-) TRUBION PHARM INC.	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307
PA	Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;	QY	301 HEAASPSQTVQRAVSNPGK 320
XX	WPI; 2005-182370/19.	DB	308 HEAASPSQTVQRAVSNPGK 327
XX	N-PSDB; ADY21798.	QY	241 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 300
XX	New non-naturally occurring single chain protein comprising polypeptides with binding domain, connecting regions and N-terminally truncated immunoglobulin, having immunological activity, useful for neutralizing infectious agent.	DB	248 NFWPDISVQMLNEVQLDPARISTTPQPKTKSGGFFVFSRLVTRAWEQKDEFTICRAV 307

QY 191 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPEWPSGRDKRTLACLIQ 240  
 DB 198 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPEWPSGRDKRTLACLIQ 247  
 QY 241 NFMPEDISVQWLHNEVQLPDRHSTTTPRKTKSGGFFVFSRLEVTAEWQKDFICRAV 300  
 DB 248 NFMPEDISVQWLHNEVQLPDRHSTTTPRKTKSGGFFVFSRLEVTAEWQKDFICRAV 307  
 QY 301 HEAASPSQTVQRAVSNPGK 320  
 DB 308 HEAASPSQTVQRAVSNPGK 327  
 RESULT 12  
 ID ADY21722 standard; protein; 331 AA.  
 AC ADY21722;  
 XX  
 DT 05-MAY-2005 (first entry)  
 DE Human IgE Fc (CH2-CH3-CH4) protein.  
 KW Antibacterial; Virucide; Antiparasitic; Fungicide; Immunotherapy;  
 KW antibody engineering; cancer; neoplasm; cytostatic; immune disorder;  
 KW graves disease; antithyroid; endocrine disease; hashimoto's disease;  
 KW immunosuppressive; rheumatoid arthritis; antiarthritic; antirheumatic;  
 KW inflammation; musculoskeletal disease; systemic lupus erythematosus;  
 KW antinflammatory; dermatological; dermatological disease;  
 KW metabolic disorder; sjogrens syndrome; ocular disease;  
 KW thrombocytopenic purpura; hemostatic; hematological disease;  
 KW multiple sclerosis; neuroprotective; neurological disease;  
 KW myasthenia gravis; muscular-gen.; bacterial infection; fungal infection;  
 KW fungicide; viral infection; virucide; parasitic infection; antiparasitic;  
 KW fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005017148-A1.  
 XX  
 PD 24-FEB-2005.  
 XX  
 PF 24-DEC-2003; 2003WO-US041600.  
 XX  
 PR 26-JUL-2003; 2003US-00627556.  
 XX  
 PA (TRUB-) TRIBION PHARM INC.  
 XX  
 PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
 XX  
 DR WPI; 2005-182370/19.  
 DR N-PSDB; ADY21721.  
 XX  
 PT New non-naturally occurring single chain protein comprising polypeptides  
 PT with binding domain, connecting regions and N-terminally truncated  
 PT immunoglobulin, having immunological activity, useful for neutralizing  
 PT infectious agent.  
 XX  
 PS Disclosure; Page 321; 590pp; English.  
 XX  
 CC The invention relates to a non-naturally occurring single chain protein  
 CC (I) comprising a first polypeptide having a binding domain polypeptide  
 CC capable of binding to a target molecule, the binding domain polypeptide  
 CC comprising a heavy chain variable region, which comprises an amino acid  
 CC substitution or deletion at one or more amino acid residues, a second  
 CC polypeptide comprising a connecting region attached to the first  
 CC polypeptide, and a third polypeptide comprising an N-terminally truncated  
 CC immunoglobulin heavy chain constant region polypeptide attached to the  
 CC second polypeptide, where the non-naturally occurring single-chain  
 CC protein is capable of an immunological activity. Also included are  
 CC reducing a target cell population in a subject (involving administering  
 CC to the subject a protein that is less than 150 kD, which involves  
 CC treating the target cell population with a first protein or peptide that

CC binds to cells within the target cell population, and treating the target  
 CC cell population with a second protein or peptide that capable of at least  
 CC one of binding an Fc receptor, inducing target cell apoptosis, or fix  
 CC complements, where the first protein or peptide molecule is directly  
 CC connected to the second protein or peptide molecule or, optionally, the  
 CC first protein or peptide molecule and the second protein or peptide  
 CC molecule are linked by a third protein or peptide molecule, and where the  
 CC protein molecule is not an antibody, a member of the TNF family or the  
 CC TNF receptor family, and is not conjugated with a bacterial toxin, a  
 CC cytotoxic drug, or a radioisotope), depleting cells in an animal  
 CC (involving administering a modified IgE protein into the blood stream of  
 CC an animal), a polynucleotide that encodes the polypeptide of the  
 CC invention, a cell containing the polynucleotide, a recombinant vector  
 CC capable of expressing the polypeptide, expressing the polypeptide, a  
 CC composition comprising the polypeptide) in combination with one or more  
 CC additional therapeutic compounds, displaying recombinant molecules (which  
 CC molecules include a native or engineered immunoglobulin heavy chain  
 CC variable region, the improvement comprising an immunoglobulin heavy chain  
 CC region that includes one or more mutation, substitution, alteration,  
 CC and/or deletion at one or more amino acid residue corresponding to  
 CC positions 9, 10, 11, 12, 108, 110, and 112 in the heavy chain variable  
 CC region) and a non-naturally occurring single chain antigen-binding  
 CC protein comprising protein having a mutation chosen from a list given in  
 CC the specification. The polypeptides of the invention comprise single  
 CC chain antibodies (scFv, with or without mutated residues) linked via an  
 CC immunoglobulin hinge region (wild-type or mutants where the cysteines are  
 CC changed to serines/prolines and denoted (SSS-PH, (CSC-S)H etc) to an  
 CC immunoglobulin (IgG, IgE or IgA) heavy chain constant region (CH) which  
 CC may also have mutations in CH2 (e.g. T256N) or a truncated CH3 (e.g. T4  
 CC CH3, a 4 amino acid deletion). The polypeptide may be further linked to a  
 CC non-antibody protein such as the transmembrane and cytoplasmic tail  
 CC (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are  
 CC useful for neutralization of an infectious agent (where the infectious  
 CC agent is a bacterium, a virus, a parasite, or a fungus) and also for  
 CC treatment of cancer, immune disorders, Grave's disease, Hashimoto's  
 CC disease, rheumatoid arthritis, systemic lupus erythematosus, Sjogren's  
 CC syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia  
 CC gravis. The present sequence is an antibody peptide or fragment (scFv,  
 CC hinge, CH region, VL or VH) used in a fusion protein of the invention.  
 XX  
 SQ Sequence 331 AA;

Query Match 100.0%; Score 1707; DB 9; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-129;  
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FTPTVKILQSSCDGGHFPPTIQLLCVSGYTPGTINITWLEDCQVMDVLDLSTASTQOE 60  
 DB 8 FTPTVKILQSSCDGGHFPPTIQLLCVSGYTPGTINITWLEDCQVMDVLDLSTASTQOE 67  
 QY 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSKKCADSNPRGVSAYLSRSPFD 120  
 DB 68 GELASTQSELTLSQKHWSLDRYTCQVYQGHTEPDSKKCADSNPRGVSAYLSRSPFD 127  
 QY 121 LFIKSPITICLVVDLAPSKGTVNLWTSRASKGPVNHSTRKEEKQNGTLTSTLPVGT 180  
 DB 128 LFIKSPITICLVVDLAPSKGTVNLWTSRASKGPVNHSTRKEEKQNGTLTSTLPVGT 187  
 QY 181 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPEWPSGRDKRTLACLIQ 240  
 DB 188 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAPEVYATPEWPSGRDKRTLACLIQ 247  
 QY 241 NFMPEDISVQWLHNEVQLPDRHSTTTPRKTKSGGFFVFSRLEVTAEWQKDFICRAV 300  
 DB 248 NFMPEDISVQWLHNEVQLPDRHSTTTPRKTKSGGFFVFSRLEVTAEWQKDFICRAV 307  
 QY 301 HEAASPSQTVQRAVSNPGK 320  
 DB 308 HEAASPSQTVQRAVSNPGK 327  
 RESULT 13  
 AAP80291

ID AAP80291 standard; protein; 367 AA.  
 XX AC AAP80291;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 06-DEC-1990 (first entry)  
 XX DE Interleukin-2/IgE Fc fusion protein.  
 XX KW Interleukin-2; IgE Fc receptor; fusion protein; asthma; dermatitis.  
 XX KW Synthetic.  
 XX OS  
 XX FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT Peptide /label= IL-2 leader sequence  
 FT Peptide 21..31  
 FT Peptide /label= IL-2 N-terminal  
 FT Peptide 32..36  
 FT Peptide /label= linker  
 FT Peptide 37..367  
 XX EP269455-A.  
 XX PN 01-JUN-1988.  
 XX PD  
 XX PF 27-NOV-1987; 87EP-00310475.  
 XX PR 28-NOV-1986; 86JP-00281871.  
 XX PR 18-SEP-1987; 87JP-00232295.  
 XX PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX PI Ikeyama S, Nishimura O;  
 XX WPI; 1988-149211/22.  
 XX Fused protein for allergy treatment - comprising interleukin-2 N-terminal  
 FT residues, a linker and human immunoglobulin E Fc fragment.  
 XX Disclosure; Page ?; 19pp; English.  
 CC This fusion protein has a low toxicity and is useful in therapy for  
 CC allergy induced by IgE. It can be used in the treatment of allergic  
 CC dermatosis, atopic dermatitis or bronchial asthma. (Updated on 25-MAR-  
 CC 2003 to correct PA field.)  
 XX SQ Sequence 367 AA;  
 Query Match 100.0%; Score 1707; DB 1; Length 367;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-129;  
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 60  
 DB 48 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 107  
 QY 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120  
 DB 108 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 167  
 QY 121 LFIKRSPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180  
 DB 168 LFIKRSPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKQKNGTLTVTSTLPVGT 227  
 QY 181 RDMIEGTYQCRVTHPLPALMRSTTKTGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
 DB 228 RDMIEGTYQCRVTHPLPALMRSTTKTGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 287  
 QY 241 NFWPEDIISVQWLHNEVLDPARHSTTQPRKTGSGFFVFSRLEVTRAENWQKDEFICRAV 300  
 DB 288 NFWPEDIISVQWLHNEVLDPARHSTTQPRKTGSGFFVFSRLEVTRAENWQKDEFICRAV 347

QY 301 HEAAPSQTQVORAVSNPGK 320  
 DB 348 HEAAPSQTQVORAVSNPGK 367  
 RESULT 14  
 AAO19666  
 ID AAO19666 standard; protein; 427 AA.  
 XX AC AAO19666;  
 XX DT 28-MAR-2003 (first entry)  
 XX DE Human IgE heavy chain constant region.  
 XX KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;  
 KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;  
 KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological;  
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.  
 XX OS Homo sapiens.  
 XX PN WO200288317-A2.  
 XX PD 07-NOV-2002.  
 XX PF 01-MAY-2002; 2002WO-US013527.  
 XX PR 01-MAY-2001; 2001US-00847208.  
 XX PR 24-OCT-2001; 2001US-00000439.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Saxon A, Zhang K, Zhu D;  
 XX WPI; 2003-103456/09.  
 XX New fusion molecules comprising polypeptide sequences that bind to IgG  
 FT inhibitory receptor and native IgE receptor, useful for treating IgE-  
 FT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
 FT autoimmune diseases.  
 XX Disclosure; Fig 5; 116pp; English.  
 CC The present invention relates to a fusion molecule comprising a first  
 CC polypeptide sequence capable of specific binding to a native IgG  
 CC inhibitory receptor consisting of an immune receptor tyrosine-based  
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
 CC functionally connected to a second polypeptide sequence capable of  
 CC specific binding directly or indirectly to a native IgE receptor  
 CC (FcepsilonR). Also provided are nucleotide sequences encoding such a  
 CC fusion protein. The fusion molecules and compositions are useful for  
 CC treating an IgE-mediated biological response, preferably an IgE-mediated  
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
 CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgE  
 CC heavy chain constant region  
 XX SQ Sequence 427 AA;  
 Query Match 100.0%; Score 1707; DB 6; Length 427;  
 Best Local Similarity 100.0%; Pred. No. 6e-129;  
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 60  
 DB 108 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQE 167  
 QY 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120

Db 168 GELASTQSELTLSQKHWLSDRYTCQVYQCHTFEDSTKKCADSNPRGVSAYLSRPSFD 227  
Qy 121 LFIKSPITICLVVDLAPSKGTVNLTWSRAGKPVNHSTRKEEKORNGTLVTSTLPVGT 180  
Db 228 LFIKSPITICLVVDLAPSKGTVNLTWSRAGKPVNHSTRKEEKORNGTLVTSTLPVGT 287  
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
Db 288 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 347  
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRLEVTRAWEOKDFICRAV 300  
Db 348 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRLEVTRAWEOKDFICRAV 407  
Qy 301 HEAASPSQTVQRAVSVNPGK 320  
Db 408 HEAASPSQTVQRAVSVNPGK 427

RESULT 15  
AAM47863  
ID AAM47863 standard; protein; 428 AA.  
XX AAM47863;  
AC  
XX  
DT 22-FEB-2002 (first entry)  
XX Human Ig-E heavy chain constant region amino acid sequence.  
DE Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;  
KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;  
KW transgenic plant.  
XX  
OS Homo sapiens.  
XX  
PN WO200183529-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 28-APR-2001; 2001WO-US013932.  
XX  
PR 28-APR-2000; 2000US-0200298P.  
XX  
PA (PLAN-) PLANET BIOTECHNOLOGY INC.  
XX  
PI Larrick JW, Wycoff KL;  
XX  
XX WPI; 2002-041481/05.  
DR N-PSDB; ABA05278.  
XX

XX Immunoadhesin for treating human rhinovirus infection comprises chimeric  
PT intercellular adhesion molecule-1, and optionally a J chain and secretory  
PT component in association.  
XX  
XX Disclosure; Fig 7; 138pp; English.  
XX  
XX The invention relates to an immunoadhesin comprising: (a) a chimeric  
CC intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor  
CC protein linked to at least a portion of an immunoglobulin heavy chain;  
CC and (b) optionally a J chain and secretory component associated with the  
CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific  
CC glycosylation and virucide activity. The immunoadhesin is useful for  
CC reducing infection by human rhinovirus (HRV) and hence the initiation or  
CC spread of the common cold by HRV. The immunoadhesin binds to HRV and  
CC reduces its infectivity, competing with cell surface ICAM-1 for binding  
CC sites, interfering with virus entry or uncoating and directing premature  
CC release of viral RNA and formation of empty capsids. Expression of the  
CC immunoadhesin in plants would be tetrameric, rather than dimeric.  
CC Immunoadhesin having multiple binding sites have a higher effective  
CC affinity for the virus, thereby increasing the effectiveness of the  
CC immunoadhesin. Association of secretory component and immunoglobulin J  
CC chain increases the stability of the immunoadhesin in the mucosal  
CC environment. Production is significantly less expensive in plants than in

CC animal cell culture and production in plants is safer for human use,  
CC since plants are not known to harbor any animal viruses. The present  
CC sequence is that of a human immunoglobulin protein sequence, useful to  
CC the invention  
XX  
SQ Sequence 428 AA;  
Query Match 100.0%; Score 1707; DB 5; Length 428;  
Best Local Similarity 100.0%; Pred. No. 6e-129;  
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FTPPTVKILSSCDGGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 60  
Db 109 FTPPTVKILSSCDGGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 168  
Qy 61 GELASTQSELTLSQKHWLSDRYTCQVYQCHTFEDSTKKCADSNPRGVSAYLSRPSFD 120  
Db 169 GELASTQSELTLSQKHWLSDRYTCQVYQCHTFEDSTKKCADSNPRGVSAYLSRPSFD 228  
Qy 121 LFIKSPITICLVVDLAPSKGTVNLTWSRAGKPVNHSTRKEEKORNGTLVTSTLPVGT 180  
Db 229 LFIKSPITICLVVDLAPSKGTVNLTWSRAGKPVNHSTRKEEKORNGTLVTSTLPVGT 288  
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
Db 289 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 348  
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRLEVTRAWEOKDFICRAV 300  
Db 349 NFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRLEVTRAWEOKDFICRAV 408  
Qy 301 HEAASPSQTVQRAVSVNPGK 320  
Db 408 HEAASPSQTVQRAVSVNPGK 428

Search completed: November 30, 2005, 00:51:24  
Job time : 154.464 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:46:45 ; Search time 30.1449 Seconds  
(without alignment)  
1021.378 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHFP.....HEAASPSQTQVRASVNVPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	428	1 EHHU	Ig epsilon chain C
2	1644.5	96.3	426	2 I36948	Ig epsilon-chain -
3	793	46.5	429	1 EHRT	Ig epsilon chain C
4	751	44.0	388	1 EHMS	Ig epsilon chain C
5	716	41.9	548	2 S38864	Ig epsilon chain C
6	678.5	39.7	423	1 EHMS	Ig epsilon chain C
7	576	33.7	227	2 PH1215	Ig epsilon chain C
8	576	33.7	243	2 PH1216	Ig epsilon chain C
9	570	33.4	115	2 E53116	Ig epsilon chain C
10	471	27.6	572	2 B46529	Ig Y heavy chain (
11	470	27.5	433	2 S31436	Ig epsilon chain -
12	469	27.5	504	2 S00390	Ig gamma chain (cl
13	455.5	26.7	549	2 S04845	Ig heavy chain pre
14	439.5	25.7	455	1 MHMS	Ig mu chain C regi
15	439.5	25.7	455	2 A24976	Ig mu chain C regi
16	433	25.4	328	2 I47158	Ig gamma 1 chain c
17	430.5	25.2	476	1 MHMS	Ig mu chain C regi
18	428.5	25.1	454	1 MHY	Ig mu chain C regi
19	428	25.1	328	2 I47161	Ig gamma 3 chain c
20	416	24.4	326	1 G2HU	Ig gamma-2 chain C
21	415	24.3	328	2 I47159	Ig gamma 2a chain
22	414	24.3	444	2 PC4436	monoclonal antibod
23	413.5	24.2	457	2 S03961	Ig mu chain C regi
24	413	24.2	453	2 S37768	Ig mu chain C regi
25	412	24.1	328	2 I47160	Ig gamma 2b chain
26	411.5	24.1	470	2 S22080	Ig heavy chain pre
27	410	24.0	391	1 MHUBT	Ig mu heavy chain
28	409.5	24.0	343	2 S25644	Ig mu chain C regi
29	409	24.0	592	2 S25705	Ig mu chain - shee

## ALIGNMENTS

### RESULT 1

BHHU

Ig epsilon chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1981 #sequence Revision 13-Jun-1983 #text Change 09-Jul-2004

C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46

R:Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene

A:Reference number: A22771; MUID:84236029; PMID:6234164

A:Accession: A22771

A:Molecule type: DNA

A:Residues: 1-428 <FLA>

A:Cross-references: UNIPROT:P01854; UNIPARC:UPI000004BB48; GB:I00022; GB:J00227; GB:V005

R:Ueda, S.; Nakai, S.; Nishida, Y.; Hsajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog

A:Reference number: A23195; MUID:84207910; PMID:6327276

A:Accession: A23195

A:Molecule type: DNA

A:Residues: 2-428 <UED>

A:Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:g184755

R:Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing

A:Reference number: PH1214; MUID:92308839; PMID:1613458

A:Accession: PH1214

A:Molecule type: DNA

A:Residues: 320-428 <ZHA>

A:Cross-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S38668; NID:g32987

R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Saeada, R.; Igarashi, K.; Kikuchi, M.; Sug

Nucleic Acids Res. 11, 719-726, 1983

A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon ch

A:Reference number: A93491; MUID:83168897; PMID:6300763

A:Accession: A93491

A:Molecule type: mRNA

A:Residues: 1-428 <SEN>

A:Cross-references: UNIPARC:UPI000004BB48; GB:I00022; GB:J00227; GB:V00555; NID:g185035

R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A:Reference number: A90824; MUID:83001945; PMID:6288268

A:Accession: A90824

A:Molecule type: DNA

A:Residues: 1-358,'L',360-428 <MAX>

A:Cross-references: UNIPARC:UPI0000173784; GB:J00222; NID:g184755

A:Note: this sequence difference may be due to polymorphism

R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-1

A:Reference number: A94418

A:Accession: A94418

A:Molecule type: protein

A;Residues: 'GAWTL', 6, 'X', 8-16, 'B', 19-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 124  
A;Cross-references: UNIPARC:UPI00000173785  
A;Experimental source: myeloma protein Nd  
R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; C  
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982  
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon  
A;Reference number: A93933; MUID:83045234; PMID:6815656  
A;Accession: B93933  
A;Molecule type: mRNA  
A;Residues: 1-40;68-114;427-428 <KEN>  
A;Cross-references: UNIPARC:UPI000001592FD; UNIPARC:UPI00000173786; UNIPARC:UPI00000173787;  
R;Keyama, S.  
FEBS Lett. 224, 306-310, 1987  
A;Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragment  
A;Reference number: S02438; MUID:98083554; PMID:3121387  
A;Accession: S02438  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 98-352 <IKE>  
A;Cross-references: UNIPARC:UPI00000173788  
R;Zhang, K.; Max, E.B.; Cheah, H.K.; Saxon, A.  
J. Biol. Chem. 269, 456-462, 1994  
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces  
A;Reference number: A53116; MUID:94103254; PMID:8276835  
A;Accession: A53116  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 320-428 <ZH2>  
A;Cross-references: UNIPARC:UPI0000014452D  
A;Experimental source: myeloma U266-derived cell line AF-10  
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)  
R;Hellman, L.  
Eur. J. Immunol. 23, 159-167, 1993  
A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of  
A;Reference number: A46536; MUID:93122085; PMID:8419166  
A;Accession: C46536  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 382-426 <HEL>  
A;Cross-references: UNIPARC:UPI00000113EF7; GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:  
A;Experimental source: B cell myeloma U-266  
A;Note: sequence extracted from NCBI backbone (NCBIP:125297)  
A;Accession: D46536  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 382-391 <HE2>  
A;Cross-references: UNIPARC:UPI00000113EF8; GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:  
A;Experimental source: B cell myeloma U-266  
A;Note: sequence extracted from NCBI backbone (NCBIP:125299)  
A;Accession: A46536  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 401-428 <HE3>  
A;Cross-references: UNIPARC:UPI00000113EF5; GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:  
A;Experimental source: B cell myeloma U-266  
A;Note: sequence extracted from NCBI backbone (NCBIP:123483)  
C;Genetics:  
A;Gene: GDB:IGHE  
A;Cross-references: GDB:119335; OMIM:147180  
A;Map position: 14q32.33-14q32.33  
A;Introns: 1/1; 104/1; 211/1; 319/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. Immunoglobulin C region; immunoglobulin homology  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F;22-87/Domain: immunoglobulin homology <IM1>  
F;128-195/Domain: immunoglobulin homology <IM2>  
F;232-301/Domain: immunoglobulin homology <IM3>  
F;338-407/Domain: immunoglobulin homology <IM4>  
F;14/Disulfide bonds: interchain (to light chain) #status predicted  
F;15-105, 295-85, 135-193, 239-299, 345-405/Disulfide bonds: #status predicted  
F;21, 49, 99, 146, 252, 275/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;121, 209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 100.0%; Score 1707; DB 1; Length 428;  
Best Local Similarity 100.0%; Pred. No. 2.2e-119; Indels 0; Gaps 0;  
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQOE 60  
DB 109 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQOE 168  
QY 61 GELASTQSELTLSQKHLSLDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120  
DB 169 GELASTQSELTLSQKHLSLDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 228  
QY 121 LFIKSKPTTICLVLDLAPSKGTVNLTWSPASGKPVNHSTRKEEKQKQNGTLTWTSTLPVGT 180  
DB 229 LFIKSKPTTICLVLDLAPSKGTVNLTWSPASGKPVNHSTRKEEKQKQNGTLTWTSTLPVGT 288  
QY 181 RDIWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTTLACLIQ 240  
DB 289 RDIWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTTLACLIQ 348  
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 300  
DB 349 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 408  
QY 301 HEAASPSTQVQRAVSNPCK 320  
DB 409 HEAASPSTQVQRAVSNPCK 428  
RESULT 2  
I36948  
IG epsilon-chain - chimpanzee (fragment)  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000  
C;Accession: I36948  
R;Sakoyama, Y.; Hong, K.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987  
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan  
A;Reference number: I36948; MUID:87147196; PMID:3103123  
A;Accession: I36948  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-426 <RES>  
A;Cross-references: UNIPARC:UPI0000011754A; GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:  
C;Genetics:  
A;Introns: 103/1; 209/1; 317/1  
A;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;336-405/Domain: immunoglobulin homology <IMW>  
Query Match 96.3%; Score 1644.5; DB 2; Length 426;  
Best Local Similarity 97.2%; Pred. No. 9.6e-115; Indels 1; Gaps 1;  
Matches 311; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
QY 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQOE 60  
DB 108 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQOE 166  
QY 61 GELASTQSELTLSQKHLSLDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120  
DB 167 GELASTQSELTLSQKHLSLDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 226  
QY 121 LFIKSKPTTICLVLDLAPSKGTVNLTWSPASGKPVNHSTRKEEKQKQNGTLTWTSTLPVGT 180  
DB 227 LFIKSKPTTICLVLDLAPSKGTVNLTWSPASGKPVNHSTRKEEKQKQNGTLTWTSTLPVGT 286  
QY 181 RDIWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTTLACLIQ 240  
DB 287 RDIWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVAFATPEWPGSRDKRTTLACLIQ 346  
QY 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 300  
DB 347 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV 406

QY 301 HBAASPSQTVORAVSNPGK 320  
 |||||  
 Db 407 HBAASPSQTVQRTVSNPGK 426  
 |||||

## RESULT 3

EHRT

Ig epsilon chain C region - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 09-Jul-2004  
 C:Accession: A93442; #sequence\_revision A02143  
 R:Hellman, L.; Petersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A:Reference number: A93442; MUID:83064537; PMID:6292865

A:Accession: A93442

A:Molecule type: mRNA

A:Residues: 1-429 <HEL>

A:CROSS-references: UNIPROT:P01855; UNIPARC:UPI000012A08F

A:Experimental source: Strain LOU/c/Wsl, immunocytoma IR2

R:Kindevoegel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.

DNA 1, 335-343, 1982

A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, i

A:Reference number: A90937; MUID:83182019; PMID:6820340

A:Contents: myeloma IR162

A:Accession: A90937

A:Molecule type: mRNA

A:Residues: 'N', 169-307, 'L', 309-342 <KIN>

A:CROSS-references: UNIPARC:UPI0000173789

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

P:19-80/Domain: immunoglobulin homology <IM1>

F:118-186/Domain: immunoglobulin homology <IM2>

F:223-291/Domain: immunoglobulin homology <IM3>

F:327-398/Domain: immunoglobulin homology <IM4>

F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.5%; Score 793; DB 1; Length 429;  
 Best Local Similarity 47.4%; Pred. No. 1.7e-51;  
 Matches 152; Conservative 54; Mismatches 109; Indels 6; Gaps 5;

QY 2 TPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWL-EDGQVMDVLDLSTASTTQOE 60  
 |||||  
 Db 101 TRPTVDLLHSSCDPNA-FHSTIQLYCFYVGHITQNDVSIHLWMDRRIYETHAQNVLIRKEE 159  
 |||||

QY 61 GELASTQSELTLSOKHWSLDRITYTCQVYQHTFEDSTKKCADSNPRGVSAYLSRPSPPD 120  
 |||||  
 Db 160 GKLASTYSLRNTTQQQWSESTFTCKVTSQGENYWAHTRRCDDBPGRVITVLIIPPSPLD 219  
 |||||

QY 121 LPIKSPITICLVLDLAPSCKGTNLTWSRASKPNVHSTRKEEKQKRNGLTITVSTLPVGT 180  
 |||||  
 Db 220 LYENGTPKLTCLVLDL-ESEENITVWVRERKSKGSASQRTKHNATTSITSLPVDA 278  
 |||||

QY 181 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTACLIQ 240  
 |||||  
 Db 279 KDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTACLIQ 337  
 |||||

QY 241 NMPEDISVQWLHNEVQLPDARHSTTPQRTKGS--FFVFSRLVTRAWEKQDEFICR 298  
 |||||  
 Db 338 NFFPEDISVQWLQDSKLIIPKSHSTTTLKNGSNQRFIFSRLEVTALWTQTQKFTCR 397  
 |||||

QY 299 AVHEAASPSQTVORAVSNPGK 319  
 |||||  
 Db 398 VIHEALRPRKLEKTIKSLG 418  
 |||||

## RESULT 4

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
 C:Accession: A02144  
 R:Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982  
 A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.  
 A:Reference number: A02144; MUID:83117774; PMID:6818553  
 A:Accession: A02144  
 A:Molecule type: mRNA

A:Residues: 1-388 <LIU>

A:CROSS-references: UNIPROT:P06336; UNIPARC:UPI000011488C; GB:J00476; NID:G194875; PIDN!

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:1-44/Domain: immunoglobulin homology (fragment) <IM1>

F:81-149/Domain: immunoglobulin homology <IM2>

F:186-254/Domain: immunoglobulin homology <IM3>

F:290-361/Domain: immunoglobulin homology <IM4>

F:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 44.0%; Score 751; DB 1; Length 388;  
 Best Local Similarity 45.8%; Pred. No. 2e-48;  
 Matches 147; Conservative 59; Mismatches 109; Indels 6; Gaps 5;

QY 2 TPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWL-EDGQVMDVLDLSTASTTQOE 60  
 |||||  
 Db 64 TEPTLELLHSSCDPNA-FHSTIQLYCFYGHILNDVSVLWMDRREITDTLTAQTVLIRKEE 122  
 |||||

QY 61 GELASTQSELTLSOKHWSLDRITYTCQVYQHTFEDSTKKCADSNPRGVSAYLSRPSPPD 120  
 |||||  
 Db 123 GKLASTCKLITEQQWSESTFTCKVTSQGVYLAHTRRCDPHEPRGVITVLIIPPSPLD 182  
 |||||

QY 121 LPIKSPITICLVLDLAPSCKGTNLTWSRASKPNVHSTRKEEKQKRNGLTITVSTLPVGT 180  
 |||||  
 Db 183 LYQNGAPKLTCLVLDLSEK-NVNVTWNQEKTSVSASQWTKHNNATTSITSLPVVA 241  
 |||||

QY 181 RDWIEGTYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTTACLIQ 240  
 |||||  
 Db 242 KDWIEGTYQCVLIDHPDPKPIVRSITKPGRSAPAEVYVFPPEE-EESDKRTTLCILQ 300  
 |||||

QY 241 NMPEDISVQWLHNEVQLPDARHSTTPQRTKGS--GFFVFSRLVTRAWEKQDEFICR 298  
 |||||  
 Db 301 NFFPEDISVQWLGDGKLIJSQHSSTTTLKNGSNQGFIFSRLEVAKLTMTQRKQFTCQ 360  
 |||||

QY 299 AVHEAASPSQTVORAVSNPGK 319  
 |||||

Db 361 VIHEALQPKRLEKTIKSLG 381  
 |||||

## RESULT 5

S38864

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001

C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of a

A:Reference number: S38864

A:Accession: S38864

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-348 <NP>

A:CROSS-references: UNIPARC:UPI00001165CC; EMBL:227397; NID:G416537; PIDN:CAA81788.1; P!

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 41.9%; Score 716; DB 2; Length 548;

Best Local Similarity 45.0%; Pred. No. 1.2e-45;

Matches 140; Conservative 56; Mismatches 101; Indels 14; Gaps 5;

QY 19 FPP-----TIQLCLVSGYTPGTINITWL-EDGQVMDVLDLSTASTTQEGELASTQS 68  
 |||||  
 |||||

Db	238	FPKPKDVLTRSTIQLCYFIYGHILNDVSVSLWMDREITDTTLAQTVLKEEGKLASTCS	297
Qy	69	ELTUSQKHLSDRYTCQVYVQGHTFEDSTKCKCADSNPRGVSAYLSRSPFDJLFIKSP	128
Db	298	KLNIITEQQMWSEFTCKVTSQGVLYLAHTRRCPDHEPRGVITYLIPPSLDLYQNGAPK	357
Qy	129	ITCLVVDLAPSKGVNLTWSRASGKPNVHSTRKEEKORNGTLTVTSTLPVGTDRDWIGET	188
Db	358	LTCLVVDLESEK-NVNVTWQEKTSVSASQWYTKHNNATTSTISLPVAKDWIEGYG	416
Qy	189	YQCRVTHPHLPRLMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPD	248
Db	417	YQCVIDHPDPKPIVRSITKTPGORSAPENVVPPPE-ESEDKRTLCLIQNFPPDIS	475
Qy	249	YQWLHNEVQLPDARHSTTPQRKTGKS--GPFVFSRLVTRAWEQKDEFICRAVHEAASP	306
Db	476	VQWLGDGLKLSNSQHSSTTTLKSGNSGRGFFISRLVRAVAKTLWTRQKQTCQVIHEALQK	535
Qy	307	SQTVQRAVSVN	317
Db	536	PRKLEKTISTS	546
EHMSS			
Ig epsilon chain C region (version 2) - mouse			
C/Species: Mus musculus (house mouse)			
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004			
C/Accession: A02145			
R/Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.			
EMBO J. 1, 1117-1123, 1982			
A/Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with human epsilon gene			
A/Reference number: A90966; MUID:84236092; PMID:6329728			
A/Accession: A02145			
A/Molecule type: DNA			
A/Residues: 1-423 <IGH>			
A/Cross-references: UNIPROT:P06336; UNIPARC:UPI000017378A			
A/Note: the sequence was determined from the germline gene			
C/Genetics:			
A/Introns: 91/1; 199/1; 307/1			
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger aggregates.			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin			
F/16-77/Domain: immunoglobulin homology <IMM1>			
F/115-183/Domain: immunoglobulin homology <IMM2>			
F/220-288/Domain: immunoglobulin homology <IMM3>			
F/325-396/Domain: immunoglobulin homology <IMM4>			
F/23-75,122-181,227-286,332-394/Disulfide bonds: #status predicted			
F/43,84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 39.7%; Score 678.5; DB 1; Length 423;			
Best Local Similarity 43.7%; Pred. No. 5.5e-43;			
Matches 136; Conservative 56; Mismatches 112; Indels 7; Gaps 6;			
Qy	13	CDGGGHPPIQLCLVSGTPTGINTWL-BGQVMDVLDLSTASTTQBELASTQSELT	71
Db	109	CDPNA-PHSTIQLCYFIYGHILNDVSVSLWMDREITDTTLAQTVLKEEGKLASTCSKLN	167
Qy	72	LSQKHLSDRYTCQVYVQGHTFEDSTKCKCADSNPRGVSAYLSRSPFDJLFIKSPITTC	131
Db	168	ITFQQMWSEFTCKVTSQGVLYLAHTRRCPDHEPRGVITYLIPPSLDLYQNGAPKLTC	227
Qy	132	LVDLAPSKGVNLTWSRASGKPNVHSTRKEEKORNGTLTVTSTLPVGTDRDWIEGETYQC	191
Db	228	LVDLESEK-NVNVTWQEKTSVSASQWYTKHNNATTSTISLPVAKDWIEGYGYQC	286
Qy	192	RVTHPHLPRLMRSTTKTS-GPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPDISVQ	250
Db	287	VDRPDPKPIVRSITLQVQSQRSAPEVYVPPPE-ESEDKRTLCLIQNFPPDISVQ	345
Qy	251	WLHNEVQLPDARHSTTPQRKTGKS--GPFVFSRLVTRAWEQKDEFICRAVHEAASPQ	308

Db	346	WLGDGKLINSQHSSTTTLKSGNSQGFIFSRLEVAKTLWTRQKQTCQVIHEALQKPR	405
Qy	309	TVORAVSVNPG	319
Db	406	KLEKTISTSIG	416
RESULT 7			
PH1215			
Ig epsilon chain C region form 2 - human (fragment)			
C/Species: Homo sapiens (man)			
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000			
C/Accession: PH1215			
R/Zhang, K.; Saxon, A.; Max, E.E.			
J. Exp. Med. 176, 233-243, 1992			
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing			
A/Reference number: PH1214; MUID:92308839; PMID:1613458			
A/Accession: PH1215			
A/Molecule type: DNA			
A/Residues: 1-227 <ZHA>			
A/Cross-references: UNIPARC:UPI0000176EFC; EMBL:X63693			
C/Genetics:			
A/Introns: 108/1; 200/3			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: alternative splicing; immunoglobulin			
F/19-88/Domain: immunoglobulin homology <IMM>			
Query Match 33.7%; Score 576; DB 2; Length 227;			
Best Local Similarity 100.0%; Pred. No. 1.1e-35;			
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	212	PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTPQRKT	271
Db	1	PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTPQRKT	60
Qy	272	KSGGFFVFSRLVTRAWEQKDEFICRAVHEAASPQTVORAVSVNPG	319
Db	61	KSGGFFVFSRLVTRAWEQKDEFICRAVHEAASPQTVORAVSVNPG	108
RESULT 8			
PH1216			
Ig epsilon chain C region form 3 - human (fragment)			
N/Alternate names: Ig epsilon chain C region, membrane-bound form (clone CH4-M2')			
C/Species: Homo sapiens (man)			
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000			
C/Accession: PH1216; D53116			
R/Zhang, K.; Saxon, A.; Max, E.E.			
J. Exp. Med. 176, 233-243, 1992			
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing			
A/Reference number: PH1214; MUID:92308839; PMID:1613458			
A/Accession: PH1216			
A/Molecule type: DNA			
A/Residues: 1-243 <ZHA>			
A/Cross-references: UNIPARC:UPI0000176EFD; EMBL:X63693			
R/Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.			
J. Biol. Chem. 269, 456-462, 1994			
A/Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces			
A/Reference number: A53116; MUID:94103254; PMID:8276835			
A/Accession: D53116			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-243 <ZH2>			
A/Cross-references: UNIPARC:UPI0000176EFD			
A/Experimental source: myeloma U266-derived cell line AF-10			
A/Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIN:141711, NCBIN:141718)			
C/Genetics:			
A/Introns: 108/1			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: alternative splicing; immunoglobulin			
F/19-88/Domain: immunoglobulin homology <IMM>			
Query Match 33.7%; Score 576; DB 2; Length 243;			

```
Best Local Similarity 100.0%; Pred. No. 1.2e-35; Indels 0; Gaps 0;
Matches 108; Conservative 0; Mismatches 0;

Qy 212 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 271
Db 1 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 60

Qy 272 KSGGFFVFSRLVTRAEWEQDEFCRAVHEAAASPSQTVQRAVSNPG 319
Db 61 KSGGFFVFSRLVTRAEWEQDEFCRAVHEAAASPSQTVQRAVSNPG 108

RESULT 9
E53116
Ig epsilon chain C region, secreted splice form (clone CH4-3'UT-CH5-M2'') - human (fragm
C:Species: Homo sapiens (man)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: E53116
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: E53116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <ZRA>
A:Cross-references: UNIPARC:UPI0000176EFF
A:Experimental source: Myeloma U266-derived cell line AP-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141720)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 33.4%; Score 570; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 212 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 271
Db 1 PRAAPEYAFATPEWPGSRDKRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT 60

Qy 272 KSGGFFVFSRLVTRAEWEQDEFCRAVHEAAASPSQTVQRAVSNP 318
Db 61 KSGGFFVFSRLVTRAEWEQDEFCRAVHEAAASPSQTVQRAVSNP 107

RESULT 10
B46529
Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: m
A:Reference number: A46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:962442; PIDN:CAA46322.1; PID
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 27.6%; Score 471; DB 2; Length 572;
Best Local Similarity 32.0%; Pred. No. 2e-27;
Matches 106; Conservative 66; Mismatches 141; Indels 18; Gaps 10;

Qy 2 TPPTVKILOSS-CDGGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVLDSTASTTQE 60
```

```
Db 248 TPPEVQLHSSVCSTLG--DSSVELLCVITGFPSPPEVEWLVG--APAHLVATMTRPQ 303
Qy 61 GELAS-----TQSELTLSOKWLSDRYTCQVY--QGHTEFDSYKKCADSNPRG---VSA 111
Db 304 REAGSKTYMATSTQNSREDWKAGKAFCTCRVKPATGCTAGHARFCFGSGAQSCSPIQI 363
Qy 112 YLSRSPFDLFIKSPPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSRTRKEEKQKRNGLT 171
Db 364 FVPPSPGSLYIQDADKVKHCLVNL-PSDASLSISWTREKSGALRPDPMLTEHPNGTFT 422
Qy 172 VTSLPVGTRDWIEGETYQCRVTHPHLPALRMSTTKTSGPRAAPEYAFATPEWPGSRD 231
Db 423 ASSSLAISTQDLAGERFTCTVQHEDLPVLGKSIKAGKAVTAPYIFTFPPHAEELSLA 482
Qy 232 KRTIACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPR-KTKGSG-FEVSRLVTRAEW 289
Db 483 EVTLTCLVRGQFQPEHVEVWLNRHNSVPAAEFVTPPLKGPNGDGTFFLYSKMTVPKASW 542
Qy 290 EOKDEFICRAVHEAAASPSQTVQRAVSNPGK 320
Db 543 QGGVSYACMVVHEGL-PMRTQRPLOKTPGK 572

RESULT 11
S31436
Ig epsilon chain - axolotl (fragment)
C:Species: Ambystoma mexicanum (axolotl)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C:Accession: S31436
R:Fellah, J.S.; Wiles, M.V.; Schwager, J.; Charlemagne, J.
submitted to the EMBL Data Library, November 1992
A:Description: cDNA sequence of Ambystoma mexicanum upelion heavy Igy chain.
A:Reference number: S31436
A:Accession: S31436
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-433 <FEL>
A:Cross-references: UNIPARC:UPI0000116C7E; EMBL:X69492; NID:962420; PID:G62421
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 27.5%; Score 470; DB 2; Length 433;
Best Local Similarity 31.0%; Pred. No. 1.7e-27;
Matches 102; Conservative 72; Mismatches 137; Indels 18; Gaps 9;

Qy 4 PTVKILQSSC---DGGHFPPTIQLCLVSGYTPGTINITWLEDQVMDVLDSTASTTQE 60
Db 111 PSVQVLQSSCADTDGNG---SIELVCLISGYTPDNIQVRLVNDKMAPIQGQTSPPQKD 166
Qy 61 GE-LASTQSELTLSOKWLSDRYTCQVYQGHY--PEDSTKKCADS-NPRGVSAYLSRP 116
Db 167 QGGTFTSTQINVTKSDWASGDKITCKVEHPATSSRAEDTTHNCADSTQTPQPKVFLAP 226
Qy 117 SPFDLFIKSPPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSRTRKEEKQKRNGLT 176
Db 227 KARDLYIANQPVVICKITKENS-DSLSTVTKRREGPEAAVISEQYIDSDGTFTAMSYL 285
Qy 177 PVGTRDWIEGETYQCRVTHPHLPALRMSTTKTSGPRAAPEYAFATPEWPGSRDKRTL 235
Db 286 NITKNEWERGDEFTCKVKHFDLPFLSRVSKPTGRSFAPTMYPVPAPEHEMELANYDFVSL 345
Qy 236 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSG---FFVFSRLVTRAEWEQ 291
Db 346 TCLVKFSFSPDDIYQWKQKGVISDKTVSNPEHQEAGTAGLGYFSYSMLTIQKSDWDK 405
Qy 292 KDEFCICRAVHEAAASPSQTVQRAVSNPGK 320
Db 406 RETFTCYAHSV-PKNLMTTRRIQKPLGK 433

RESULT 12
S00390
Ig gamma chain (clone 36) - chicken (fragment)
```



A;Cross-references: UNIPARC:UPI00001737BB  
C;Genetics:  
A;Introns: 1/1; 106/1; 219/1; 325/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F;21-91/Domain: immunoglobulin homology <IMM1>  
F;129-201/Domain: immunoglobulin homology <IMM2>  
F;239-307/Domain: immunoglobulin homology <IMM3>  
F;346-417/Domain: immunoglobulin homology <IMM4>  
F;436-455/Domain: carboxyl-terminal <CTS>  
F;14/Disulfide bonds: interchain (to light chain) #status predicted  
F;46,211,243,281,442/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;28-89/Disulfide bonds: #status experimental  
F;136-199,246-305,353-415/Disulfide bonds: #status predicted  
F;216,454/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;293/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 25.7%; Score 439.5; DB 1; Length 455;  
Best Local Similarity 32.3%; Pred. No. 3.4e-25; Mismatches 152; Indels 13; Gaps 8;  
Matches 106; Conservative 57;

QY 4 PTVKILQSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQGE 62  
DB 112 PNVNVPVPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKGKLVESGFTTDPVTIENK 171

QY 63 LASTQ-----SELTLSQKHWLSDRYTCQVYQGHFT-EDSTKKCADSNPRGVSAYLRSR 116  
DB 172 GSTPQYKVIISTLTISEIDWLNLVYTCRDVHRLGTLFLKNVSSSTCAASPSTDLTFTIPP 231

QY 117 SPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKQNGTLTSTL 176  
DB 232 SFADIFLSKANLTLCLVSNLATYE-TLNIWASQSGEPLETKIKIMESHHPNGTFSAKGVA 290

QY 177 PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKSGPRAAPEVYAFATP--EWPGRDKRT 234  
DB 291 SVCVEDWNRKEFVCTVTHRDLPSPQKFKISKPNVHKHPPAVYLLPPAREQLNRESAT 350

QY 235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGF-FVFSRLEVTVAEWEQK 292  
DB 351 VTCLVKGFSPADISVQWLQRLPQEKYVTSAPMPGPAGFYFTHSILITVTEEMNSG 410

QY 293 DEFICRAVHEAASPSQTVQRAVSNPGK 320  
DB 411 ETYTCVVGHEAL-PHLVTERTVDKSTGK 437

RESULT 15  
A24976  
Ig mu chain C region (allele b) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 21-Jan-2000  
C;Accession: A24976  
R;Schreier, P.H.; Quester, S.; Rothwell, A.  
Nucleic Acids Res. 14, 2381-2389, 1986  
A;Title: Allotypic differences in murine mu-genes.  
A;Reference number: A24976; MUID:86176735; PMID:3083402  
A;Accession: A24976  
A;Molecule type: mRNA  
A;Residues: 1-455 <SCH>  
A;Cross-references: UNIPARC:UPI0000115D47; GB:X03690; NID:952381; PIDN:CAA27326.1; PID:9  
A;Experimental source: strain C57BL/6  
A;Note: the authors translated the codon AAG for residue 65 as Leu  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;346-417/Domain: immunoglobulin homology <IMM>

Query Match 25.7%; Score 439.5; DB 2; Length 455;  
Best Local Similarity 32.3%; Pred. No. 3.4e-25; Mismatches 152; Indels 13; Gaps 8;  
Matches 106; Conservative 57;

QY 4 PTVKILQSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQGE 62

DB 112 PNVNVPVPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKGKLVESGFTTDPVTIENK 171  
QY 63 LASTQ-----SELTLSQKHWLSDRYTCQVYQGHFT-EDSTKKCADSNPRGVSAYLRSR 116  
DB 172 GSTPQYKVIISTLTISEIDWLNLVYTCRDVHRLGTLFLKNVSSSTCAASPSTDLTFTIPP 231  
QY 117 SPFDLFIKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKQNGTLTSTL 176  
DB 232 SFADIFLSKANLTLCLVSNLATYE-TLNIWASQSGEPLETKIKIMESHHPNGTFSAKGVA 290  
QY 177 PVGTRDWIEGETYQCRVTHPHLPRALMRSTTKSGPRAAPEVYAFATP--EWPGRDKRT 234  
DB 291 SVCVEDWNRKEFVCTVTHRDLPSPQKFKISKPNVHKHPPAVYLLPPAREQLNRESAT 350  
QY 235 LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGF-FVFSRLEVTVAEWEQK 292  
DB 351 VTCLVKGFSPADISVQWLQRLPQEKYVTSAPMPGPAGFYFTHSILITVTEEMNSG 410

QY 293 DEFICRAVHEAASPSQTVQRAVSNPGK 320  
DB 411 ETYTCVVGHEAL-PHLVTERTVDKSTGK 437

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Job time : 31.1449 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:43:39 ; Search time 176.232 Seconds  
(without alignments)  
1281.091 Million cell updates/sec

Title: US-09-847-208B-6  
Perfect score: 1707  
Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPSQTVQRAVSNVPGK 320

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05\_80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	1707	100.0	428	1 IGHE_HUMAN	P01854 homo sapien
2	793	46.5	429	1 IGHE_RAT	P01855 rattus norv
3	751	44.0	421	1 IGHE_MOUSE	P08336 mus musculu
4	459.5	26.9	560	2 Q4V801_XENLA	Q4V801 xenopus lae
5	448.5	26.3	337	2 Q95M34_HORSE	Q95M34 equus cabal
6	439.5	25.7	454	1 MUC_MOUSE	P01872 mus musculu
7	439.5	25.7	590	2 Q4V9V8_MOUSE	Q4V9V8 mus musculu
8	434.5	25.5	617	2 Q4KML5_MOUSE	Q4KML5 mus musculu
9	431.5	25.3	614	2 Q7TMT6_MOUSE	Q7TMT6 mus musculu
10	430.5	25.2	475	1 MUC_MOUSE	P01873 mus musculu
11	430.5	25.2	613	2 Q8VCX7_MOUSE	Q8VCX7 mus musculu
12	430.5	25.2	616	2 Q504M7_MOUSE	Q504M7 mus musculu
13	426	25.0	464	2 Q6MZU6_HUMAN	Q6mzu6 homo sapien
14	423.5	24.8	454	1 MUC_MESAU	P06337 mesocricetu
15	421	24.7	465	2 Q6P6C4_HUMAN	Q6P6C4 homo sapien
16	420	24.6	417	2 Q6N093_HUMAN	Q6N093 homo sapien
17	417	24.4	470	2 Q68CN4_HUMAN	Q68CN4 homo sapien
18	416	24.4	326	1 IGHG2_HUMAN	P01859 homo sapien
19	414	24.3	458	2 Q65ZQ1_HUMAN	Q65ZQ1 homo sapien
20	413.5	24.2	457	1 MUC_SUNMU	P20768 suncus muri
21	413	24.2	375	2 Q86TT1_HUMAN	Q86TT1 homo sapien
22	413	24.2	463	2 Q99LC4_MOUSE	Q99LC4 mus musculu
23	413	24.2	597	2 Q9BU10_HUMAN	Q9BU10 homo sapien
24	413	24.2	597	2 Q9QB88_HUMAN	Q9QB88 homo sapien
25	413	24.2	597	2 Q96BB9_HUMAN	Q96BB9 homo sapien
26	413	24.2	597	2 Q6GMX5_HUMAN	Q6gmX5 homo sapien
27	413	24.2	606	2 Q6GMY2_HUMAN	Q6gmy2 homo sapien
28	410.5	24.0	371	2 Q5RK07_RAT	Q5RK07 rattus norv
29	410.5	24.0	590	2 Q569B8_RAT	Q569B8 rattus norv
30	410.5	24.0	591	2 Q510L9_RAT	Q510L9 rattus norv
31	410.5	24.0	591	2 Q4QW0_RAT	Q4qqw0 rattus norv

32 410.5 24.0 598 2 Q568Y0\_RAT Q568Y0 rattus norv  
33 410 24.0 391 1 MUCB\_HUMAN P04220 homo sapien  
34 405.5 23.8 454 1 MUC\_HUMAN P01871 homo sapien  
35 405.5 23.8 458 1 MUC\_RABIT P03988 oryctolagus  
36 404.5 23.7 329 1 IGHG2\_CAVPO P01862 cavia porce  
37 404 23.7 464 2 Q6PF95\_MOUSE Q6pf95 mus musculu  
38 404 23.7 472 2 Q6N089\_HUMAN Q6n089 homo sapien  
39 404 23.7 595 2 Q8WUX4\_HUMAN Q8wux4 homo sapien  
40 404 23.7 613 2 Q8WUK1\_HUMAN Q8wuk1 homo sapien  
41 404 23.7 620 2 Q96EY0\_HUMAN Q96ey0 homo sapien  
42 404 23.7 625 2 Q96AA6\_HUMAN Q96aa6 homo sapien  
43 402 23.6 324 1 IGHG1\_MOUSE P01868 mus musculu  
44 402 23.6 464 2 Q6PIP8\_MOUSE Q6pip8 mus musculu  
45 402 23.6 465 2 Q6PJB2\_MOUSE Q6pjb2 mus musculu

## ALIGNMENTS

## RESULT 1

IGHE\_HUMAN STANDARD; PRT; 428 AA.  
ID IGHE\_HUMAN  
AC P01854;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig epsilon chain C region.  
GN Name=IGHE;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83168897; PubMed=6300763;  
RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,  
RA Kikuchi M., Sugino Y., Nishida Y., Honjo T.;  
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin  
RT epsilon chain cDNA";  
RL Nucleic Acids Res. 11:719-726(1983).  
RN [2]  
RP NUCLEOTIDE SEQUENCE, AND VARIANT LEU-359.  
RX MEDLINE=83001945; PubMed=6288268; DOI=10.1016/0092-8674(82)90185-4;  
RA Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;  
RT "Duplication and deletion in the human immunoglobulin epsilon genes.";  
RL Cell 29:691-699(1982).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84236029; PubMed=6234164;  
RA Flanagan J.G., Rabbitts T.H.;  
RT "The sequence of a human immunoglobulin epsilon heavy chain constant  
RT region gene, and evidence for three non-allelic genes.";  
RL EMBO J. 1:1655-660(1982).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84207910; PubMed=6327276;  
RA Ueda S., Nakai S., Nishida Y., Hiseajima H., Honjo T.;  
RT "Long terminal repeat-like elements flank a human immunoglobulin  
RT epsilon pseudogene that lacks introns";  
RL EMBO J. 1:1539-1544(1982).  
RN [5]  
RP PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).  
RX Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;  
RL (In) Bach M.K. (eds.);  
RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,  
RL Marcel Dekker, New York (1978).  
RN [6]  
RP NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428.  
RX MEDLINE=83065234; PubMed=6815856;  
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,  
RA Bell L.O., Gould H.J.;  
RT "Cloning and sequence determination of the gene for the human



NCBI\_TaxID=10116;  
[1]  
RN NUCLEOTIDE SEQUENCE (IMMUNOCYTOMA IR2).  
RC STRAIN=LOU/C/WSL;  
RA MEDLINE=83064537; PubMed=6292865;  
RX Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;  
RT "Structure and evolution of the heavy chain from rat immunoglobulin  
E.";  
RL Nucleic Acids Res. 10:6041-6049(1982).  
[2]  
RN NUCLEOTIDE SEQUENCE OF 168-342 (MYELOMA IR162).  
RX MEDLINE=83182019; PubMed=6820340;  
RA Kindvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;  
RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:  
RT construction, identification, and DNA sequence.";  
RL DNA 1:335-343(1982).  
[3]  
RN NUCLEOTIDE SEQUENCE OF 205-306.  
RX MEDLINE=82174576; PubMed=6803238;  
RA Hellman L., Pettersson U., Bennich H.;  
RT "Characterization and molecular cloning of the mRNA for the heavy  
RT (epsilon) chain of rat immunoglobulin E.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).  
CC -!- SIMILARITY: Contains 4 Ig-like (immunoglobulin-like) domains.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; J00744; AAA41379.1; ALT\_INIT; mRNA.  
DR PIR; A93442; EHRT.  
DR HSSP; P01854; IFFS.  
DR Ensembl; ENSRNOG000005328; Rattus norvegicus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; Cl-set; 2.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; IGc1; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.  
FT DOMAIN 6 89  
FT Ig-like 1.  
FT DOMAIN 103 201  
FT Ig-like 2.  
FT DOMAIN 205 305  
FT Ig-like 3.  
FT DOMAIN 314 414  
FT Ig-like 4.  
FT R -> N (in Ref. 2).  
FT P -> L (in Ref. 2).  
FT CONFLICT 168 168  
FT 308 308  
FT NON\_TER 1  
FT SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;  
SQ  
Query Match 46.5%; Score 793; DB 1; Length 429;  
Best Local Similarity 47.4%; Pred. No. 3.7e-55;  
Matches 152; Conservative 54; Mismatches 109; Indels 6; Gaps 5;  
QY 2 TPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWL-EDGQVMDVLSSTATTQ 60  
DB 101 TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHQNDVSIHLMDDRKIVETHAQNVLKEE 159  
QY 61 GELASTQSELTISQKHLSDRYTCQVYQGHFTFEDSTKCKADSNPRGVSAYLSRPSPD 120  
DB 160 GKLASTYSRLNITQQQWMESESTFTCKVTSQGENYWAHTRCRSDDEPRGVITLYLIPSP 219  
QY 121 LFRKSPPTICLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQNGTLTWTSTLPVGT 180  
DB 220 LYENGTFPKLTCVLVDL-ESEENITVTWVRERKKSIGSASQRTKHNATTSISLPVDA 278  
QY 181 RWIEGEGTQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
DB 279 KOWIEGEGTQCRVDHFFHFKPIVRSITKAPGRSAPEVYVFLPPE-EEEKDKRTLTCLIQ 337

QY 241 NFMPEDISVQWLHNEVQLPDARHSTTPQPRKTKSG--FFVFSRLVETRAWEQKDEFTCR 298  
DB 338 NFFPEDISVQWLQDSKLIPKSHQSTTTPLKYNQSNORFFFSRLVETKALMTQTKQFTCR 397  
QY 299 AVHEAASPSQTVORAVSVNFG 319  
DB 398 VIHEALREPRKLERITISKSLG 418  
RESULT 3  
IGHE\_MOUSE STANDARD; PRT; 421 AA.  
ID IGHE\_MOUSE  
AC P06336; P01856;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig epsilon chain C region.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=84236092; PubMed=6329728;  
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;  
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:  
RT comparison with the human epsilon gene sequence.";  
RL EMBL J. 1:1117-1123(1982).  
[2]  
RN SEQUENCE REVISION.  
RP Honjo T.;  
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.  
[3]  
RN NUCLEOTIDE SEQUENCE OF 34-421.  
RX MEDLINE=8311774; PubMed=6818553;  
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;  
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain  
RT cDNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; X01857; CAA25977.1; -; Genomic DNA.  
DR EMBL; X01857; CAA25978.1; -; Genomic DNA.  
DR PIR; A02144; EHMS.  
DR PIR; A02145; EHMS.  
DR HSSP; P01854; IFFS.  
DR Ensembl; ENSMUSG000000021153; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; Cl-set; 1.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGc1; 2.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; 3.  
KW Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.  
FT REGION 1 90  
FT CH1.  
FT REGION 91 197  
FT CH2.  
FT REGION 198 304  
FT CH3.  
FT REGION 305 421  
FT CH4.  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 43 43  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 72 72  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 84 84  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 95 95  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 166 166  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 238 238  
FT N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 261 261  
FT N-linked (GlcNAc... ) (Potential).

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FT CARBOHYD 365 365 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 415 415 N-linked (GlcNAc... ) (Potential).
FT DISULFID 23 75 By similarity.
FT DISULFID 121 180 By similarity.
FT DISULFID 226 285 By similarity.
FT DISULFID 330 392 By similarity.
FT NON TER 1 1
SQ SEQUENCE 421 AA; 47321 MW; 8F909E1F30A06B47 CRC64;

Query Match 44.0%; Score 751; DB 1; Length 421;
Best Local Similarity 45.8%; Pred. No. 8.6e-52;
Matches 147; Conservative 59; Mismatches 109; Indels 6; Gaps 5;

QY 2 TPTVKILQSCDGGHPPPTIQLLCLVSGYTGTTNITWL-EDGQVMDVLDSTASTQGE 60
DB 97 TEPTLELHSSCDPNA-FHSTIQLYCFIYGHILNDVSVWLMDREITDTLAQTVLKKE 155
QY 61 GELASTQSELTLSQKHLSDRTYTCOVYQGHFTFEDSTKKCADSPRGVSAYLSRPSFD 120
DB 156 GKLASTCSKLNITEQQWMSSTFTCKVISQGVYLAHTRCPDHEPRGVITYLIPSPLD 215
QY 121 LFIKRSPTITCLVVDLAPSKGTVNLTWRSAGKPVNHSTRKEBKQRNGTLTVTSTLPVGT 180
DB 216 LYQNGAPKLCVVDLESER-NNVNTWNEKKTSSVSASQWYTKHNNATTSTSLPVVA 274
QY 181 RDWIEGTQYCRVTHPHLPALMRSTTKTGSPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
DB 275 KDWIEGYGYCIVDHPDPFKPIVRISITKTPQRSAPENVYVFPFPE-EESDKRTLCLIQ 333
QY 241 NFWPDISVQWLHNEVOLPDARHSTTTPRKTKGS--GFFVFSRLVETRAEWEQKDSFICR 298
DB 334 NFPEDISVQWLHNEVOLPDARHSTTTPRKTKGS--GFFVFSRLVETRAEWEQKDSFICR 298
QY 299 AVHEAASPSQTVQRAVSNPG 319
DB 394 VIHEALQKPRKLEKTIISTSLG 414

RESULT 4
Q4V801 XENLA PRELIMINARY; PRT; 560 AA.
AC Q4V801;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE LOC398774 protein.
GN Names=LOC398774;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.D., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Siemen C.M., Schuler G.D.,
RA Atlshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
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RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL SUBMITTED (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC097629; AAH97629.1; -, mRNA.
SQ SEQUENCE 560 AA; 61795 MW; 9DED2DD2B17CFDBE CRC64;

Query Match 26.9%; Score 459.5; DB 2; Length 560;
Best Local Similarity 33.1%; Pred. No. 3.2e-28;
Matches 107; Conservative 60; Mismatches 137; Indels 19; Gaps 9;

QY 4 PTVKILQSCDGGHPPPTIQLLCLVSGYTGTTNITWLQEDQVMDVLDSTAS-TTQEGE 62
DB 251 PTVKILQSCASS-----ESVELLCLITYAPSEIKVQWLNQGVTEISPSNKPCKEEND 306
QY 63 LASTQSELTLSQKHLSDRTYTCOVYQGHFT-FEDSTKKCADS--NPRGVSAVLSRPS 118
DB 307 TFSRSKSVKVPKEDWNSGDSYTKVTHPASHYKTEASTKKDDTAITPK---VDVLPPSP 363
QY 119 FDLFIKRSPTITCLVVDLAPSKGTVNLTWRSAGKPVNHSTRKEBKQRNGTLTVTSTLPV 178
DB 364 KDLVTKKAKVYC-VISRMTSDDLTVQWSRSDGKKALAFDSAPKAYDGTFTVKSTLKI 422
QY 179 GTRDWIEGTQYCRVTHPHLPALMRSTTKTGSPRAAPEVYAFATPEWPGSRDKRTLACL 238
DB 423 SPGDWENKQFNCKVQVHPDLPSPIEKSIQKSDQPGTEPTITLLPPSDDELNDIFSLICW 482
QY 239 IONFMPEDISVQWLHNEVOLPDARHSTTTPRKTKGSFFVFSRLVETRAEWEQKDEFIC 297
DB 483 LKNFRPQDIYVFWKDGVTLEEDYNTTTPVLEEEEGFISFKLTIARSDWNRGATYSC 542
QY 298 RAVHEAASPSQTVQRAVSNPG 320
DB 543 IAAHNTIS-----QRDIKKNRGK 560

RESULT 5
Q95M34 HORSE PRELIMINARY; PRT; 337 AA.
ID Q95M34 HORSE PRELIMINARY;
AC Q95M34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (fragment).
GN Name=IGHC1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RL genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RN Immunobiology 199:105-118(1998).
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22172648; PubMed=12185539; DOI=10.1007/s00251-002-0458-4;
```

RA Wagner B., Greiser-Wilke I., Wege A.K., Radbruch A., Leibold W.;  
RT "Evolution of the six horse IGHG genes and corresponding  
RL immunoglobulin gamma heavy chains.";  
DR EMBL; AJ300675; CAC44624.1; -; mRNA.  
DR HSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF07654; CI-set; 3.  
DR SMART; SM00407; IGC1; 2.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; UNKOWN 2.  
FT CHAIN <1 337 immunoglobulin gamma 1 heavy chain  
FT NON TER 1  
FT SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;  
SQ  
Query Match 26.3%; Score 448.5; DB 2; Length 337;  
Best Local Similarity 31.3%; Pred. No. 1.3e-27;  
Matches 106; Conservative 62; Mismatches 146; Indels 25; Gaps 8;  
QY 2 TPPTVKILQSSGCGGHPPTIQLCLVSGYTPGTINITWLEDGQWMDVLTSTATTQEG 61  
Db 4 TAPKVFALPGC--GTTSDITVALGCLVSGYFPFEPVKVSW-NSGSLTSGVHTFPSVLQSS 60  
QY 62 ELASTQSELTLSQKWLSDRTYTCQVYQGHTE-----DSTKKCADSN--PR--- 107  
Db 61 GFYSLSMVTVPASTWTSE-TYICNVVHAASNFKVDKRIEPIPDNHQKVCMSKCPKCPA 119  
QY 108 -----GVSAIYLRSPED-LFIRKSPITITCLVDLAPSKGTWNLVTSRASGKPVNHSRK 161  
Db 120 BELLGGSPVFPFPKPKMTITRPEVTCVVDVSVQENPDVKFNWMDGVEVTRATRP 179  
QY 162 BEKQNGTLTVTSLFVGTDRWIEGETYQCRVTHPLPALMRSTTKTGPPRAPEVYAF 221  
Db 180 KEEQFNSTYRVVSVLRIHQDWLSGKEFKCKVNNQALPQIERTITTKGRSQEPQVYVL 239  
QY 222 ATPWPGGRDKTACLQNFPEDISVQWLNHNEVQLDPARHSTTPQRTKSGGFVFSR 281  
Db 240 APHPDELKSKSVTCLVKDFPYPINIEWQSNQGOPELETKYSTTAAQSDSGSYFLYSK 299  
QY 282 LEVTRAWEQKDEFICRAVHEAASPSQTVORAVSNPGK 320  
Db 300 LSVDRNRWQGGTTFTCGVWHEALHNHYT-QKNVSNKPGK 337  
RESULT 6  
MUC\_MOUSE  
ID MUC\_MOUSE STANDARD; PRT; 454 AA.  
AC P01872;  
DC 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-2005 (Rel. 46, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig mu chain C region secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=81076590; PubMed=6255422;  
RA Kawakami T., Takahashi N., Honjo T.;  
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and  
RT comparison with other immunoglobulin heavy chain genes.";  
RL Nucleic Acids Res. 8:3933-3945(1980).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=82051295; PubMed=6795090; DOI=10.1016/0378-1119(81)90102-5;  
RA Goldberg G.I., Vanin B.F., Zrolka A.M., Blattner F.R.;  
RT "Sequence of the gene for the constant region of the mu chain of  
RT Balb/c mouse immunoglobulin.";

RL Gene 15:33-42(1981).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (MVELOMA TEPC183).  
RX MEDLINE=81155562; PubMed=6260591; DOI=10.1016/0378-1119(80)90017-7;  
RA Auffray C., Rougeon F.;  
RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu  
RT chain of mouse immunoglobulin.";  
RL Gene 12:77-86(1980).  
RN [4]  
RP PROTEIN SEQUENCE (MVELOMA PROTEIN MOPC 104E).  
RX MEDLINE=79223904; PubMed=111247;  
RA Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.;  
RT "Amino acid sequence of a mouse immunoglobulin mu chain.";  
RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).  
RN [5]  
RP SEQUENCE REVISION (MOPC 104E).  
RX MEDLINE=83075344; PubMed=6816276;  
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
RT Hood L.E.;  
RL "Complete amino acid sequence of a mouse mu chain: homology among  
RT heavy chain constant region domains.";  
RL Biochemistry 21:5415-5424(1982).  
CC -|- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Comment=During differentiation, B lymphocytes switch from  
CC expression of isoform Membrane-bound to isoform Secreted;  
CC Name=Secreted;  
CC IsoId=P01872-1; Sequence=Displayed;  
CC Name=Membrane-bound;  
CC IsoId=P01873-1; Sequence=External;  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; J00443; AAB59650.1; -; Genomic DNA.  
CC EMBL; J00444; AAB59650.1; JOINED; Genomic\_DNA.  
CC EMBL; V00827; -; NOT\_ANNOTATED\_CDS; mRNA.  
CC PIR; A02166; MHMS.  
CC HSSP; P01861; IADQ.  
CC Ensembl; ENSMUSG00000054328; Mus musculus.  
CC GO; GO:0019815; C:B cell receptor complex; IDA.  
CC GO; GO:0009897; C:external side of plasma membrane; IDA.  
CC GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
CC GO; GO:0048471; C:perinuclear region; IDA.  
CC GO; GO:0003823; F:antigen binding; IDA.  
CC GO; GO:0005515; F:protein binding; IPI.  
CC GO; GO:0004888; F:transmembrane receptor activity; IDA.  
CC GO; GO:0000187; P:activation of MAPK; IDA.  
CC GO; GO:0030333; P:antigen processing; IDA.  
CC GO; GO:0050853; P:B cell receptor signaling pathway; IDA.  
CC GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
CC GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.  
CC GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.  
CC GO; GO:0045807; P:positive regulation of endocytosis; IDA.  
CC GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . . ; IDA.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003597; Ig cl.  
CC Pfam; PF07654; CI-set; 4.  
CC SMART; SM00407; IGC1; 4.  
CC PROSITE; PS50835; IG\_LIKE; 4.  
CC PROSITE; PS00290; IG\_MHC; 3.  
KW Alternative splicing; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT REGION <1 104  
FT REGION 105 216  
FT REGION 217 323  
FT REGION 324 435  
FT REGION 436 454  
FT C-terminal segment of secreted form.

FT CARBOHYD 45 45 N-linked (GlcNAc...)  
 FT CARBOHYD 210 210 N-linked (GlcNAc...)  
 FT CARBOHYD 242 242 N-linked (GlcNAc...)  
 FT CARBOHYD 280 280 N-linked (GlcNAc...)  
 FT CARBOHYD 441 441 N-linked (GlcNAc...)  
 FT DISULFID 13 13 Interchain (with light chain) (Probable).  
 FT DISULFID 27 27 Interchain (with light chain) (Probable).  
 FT DISULFID 135 135 By similarity.  
 FT DISULFID 215 215 Interchain (with heavy chain) (Probable).  
 FT DISULFID 245 245 By similarity.  
 FT DISULFID 292 292 Interchain (with heavy chain) (Probable).  
 FT DISULFID 352 352 By similarity.  
 FT DISULFID 453 453 Interchain (with heavy chain) (Probable).  
 FT VARIANT 77 77 S -> N (in MOPC 104E).  
 FT VARIANT 100 100 H -> Q (in MOPC 104E).  
 FT VARIANT 225 225 T -> N (in TPC183 and MOPC 104E).  
 FT VARIANT 257 257 N -> S (in TPC183).  
 FT VARIANT 257 257 N -> T (in MOPC 104E).  
 FT VARIANT 367 367 L -> K (in TPC183 and MOPC 104E; requires 2 nucleotide substitutions).  
 FT NON TER 1 1  
 SQ SEQUENCE 454 AA; 49972 MW; EBCCA6B8569AEEC5 CRC64;  
 Query Match 25.7%; Score 439.5; DB 1; Length 454;  
 Best Local Similarity 32.3%; Pred. No. 9.8e-27;  
 Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;  
 QY 4 PTVKILQSSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQGE 62  
 DB 111 PNVNVPVPRDGFSGPAPRKSLICEATNTPKPIVSWLKDGLVESGFTDPVTIENK 170  
 QY 63 LASTQ-----SELTLSQKHLSDRTYTCQVYQGHF-EDSTKKCADSNPRGVSAYLSRP 116  
 DB 171 GSTPQTYKVISTLTISEIDNLNLYVTCRVDHRGLTFLKNVSTCAASPSDILTFTIPP 230  
 QY 117 SPFDLFRKSPITICLVLDLAPSKGTNLTWSRASKGPNVHSTRKEEKQNGTLTVTSTL 176  
 DB 231 SFADIFLSKANLTCVLSNLTATYE-TLNISWASQSGEPLTKIKIMESHNGFTSAKVA 289  
 QY 177 PVGTRDWIEGETYQCRVTHPLRALMRSTTKTSGPRAAPEVYAFATP--EWPGRDKRT 234  
 DB 290 SVCVEDNNRKEFVCTVTRDLPSQPKFKISKNEVHKHPAVYLLPPAREQLNRESAT 349  
 QY 235 LACIQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKGS-GF-FVFSRLVETRAWEOK 292  
 DB 350 VTCLVKGFSPADISVQWLQRLLPQEKYVTSAPMPEPGAGFYFTHSILTVTEEWNSG 409  
 QY 293 DEFTICRAVHEAASPSQTVORAVSNPGK 320  
 DB 410 ETTYTCVVGHEAL-PHLVTERTVDKSTGK 436

RESULT 7  
 Q4V9V8\_MOUSE PRELIMINARY; PRT; 590 AA.  
 ID Q4V9V8\_MOUSE PRELIMINARY; PRT; 590 AA.  
 AC Q4V9V8;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=Igh-6;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RG NIH MGC Project;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC096667; AAH96667.1; -; mRNA.  
 DR MGI; MGI:96448; Igh-6.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF07654; C1-set; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;  
 Query Match 25.7%; Score 439.5; DB 2; Length 590;  
 Best Local Similarity 32.3%; Pred. No. 1.4e-26;  
 Matches 106; Conservative 57; Mismatches 152; Indels 13; Gaps 8;  
 QY 4 PTVKILQSSCDG-GGHFPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQGE 62  
 DB 247 PNVNVPVPRDGFSGPAPRKSLICEATNTPKPIVSWLKDGLVESGFTDPVTIENK 306  
 QY 63 LASTQ-----SELTLSQKHLSDRTYTCQVYQGHF-EDSTKKCADSNPRGVSAYLSRP 116  
 DB 307 GSTPQTYKVISTLTISEIDNLNLYVTCRVDHRGLTFLKNVSTCAASPSDILTFTIPP 366  
 QY 117 SPFDLFRKSPITICLVLDLAPSKGTNLTWSRASKGPNVHSTRKEEKQNGTLTVTSTL 176  
 DB 367 SFADIFLSKANLTCVLSNLTATYE-TLNISWASQSGEPLTKIKIMESHNGFTSAKVA 425  
 QY 177 PVGTRDWIEGETYQCRVTHPLRALMRSTTKTSGPRAAPEVYAFATP--EWPGRDKRT 234  
 DB 426 SVCVEDNNRKEFVCTVTRDLPSQPKFKISKNEVHKHPAVYLLPPAREQLNRESAT 485  
 QY 235 LACIQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKGS-GF-FVFSRLVETRAWEOK 292  
 DB 486 VTCLVKGFSPADISVQWLQRLLPQEKYVTSAPMPEPGAGFYFTHSILTVTEEWNSG 545  
 QY 293 DEFTICRAVHEAASPSQTVORAVSNPGK 320  
 DB 546 ETTYTCVVGHEAL-PHLVTERTVDKSTGK 572  
 RESULT 8  
 Q4KML5\_MOUSE PRELIMINARY; PRT; 617 AA.  
 ID Q4KML5\_MOUSE PRELIMINARY; PRT; 617 AA.  
 AC Q4KML5;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RG NIH MGC Project;  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC098504; AAH98504.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;  
Query Match 25.5%; Score 434.5; DB 2; Length 617;  
Best Local Similarity 32.6%; Pred. No. 3.7e-26;  
Matches 105; Conservative 54; Mismatches 150; Indels 13; Gaps 8;  
QY 4 PTVKILQSSCDG-GGHPPTTQLCLVSGYTPGTINITWLEDQVMDVLSTASTQGE 62  
Db 253 PNVNFFVPPRDGFGSPAPRKSCLICEATNFTPKITVSWLKDGLVSGFTTDPVTIENK 312  
QY 63 LASTQ-----SELTLSQKHLSDRITYTCOVYQGHFT-EDSTKKCADSNPRGVSAYLSRP 116  
Db 313 GSTPQTYKVIISTLTISEIDMLNVLNYTCRVDRHGLTFLRDVSTCAASPSTDLITFTIPP 372  
QY 117 SPFDLFIKRSPTITCLVVDLAPSKGTVNLTWSRASKPVNHSRKEEKQKNGTLTSTL 176  
Db 373 SFADIFLSKSNLTCLVSNLAYE-TLNIWSASQSGEPLTKIKIMESHNPCTFSAGVA 431  
QY 177 PVGTRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYATP--EWPGRDRKRT 234  
Db 432 SVCVEDMNNRKEFVCTVTHRLDLPSPQKKFISKPNVHKHPVAVYLLPPAREQLNRESAT 491  
QY 235 LACLQNFNPEDISVOWLHNEVQLPDARHSTTQPKTKGS-GF-FVFSLEVTAEWEQK 292  
Db 492 VTCLVKGFSPADISVOWLQGLLPQEKYVTSAPMPGAPGFYFTHSILTVTEBWSNG 551  
QY 293 DEFICRAVHEAASPQTVORAV 314  
Db 552 EYTCVVGHEAL-PHLVTERTV 572  
RESULT 9  
Q7TWT6 MOUSE  
ID Q7TWT6\_MOUSE PRELIMINARY; PRT; 614 AA.  
AC Q7TWT6;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE MG60843 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC053409; AAH53409.1; -; mRNA.  
DR HSSP; P01820; IG7J.  
DR Ensembl; ENSMUSG00000054328; Mus musculus.  
DR GO; GO:0003823; F:antigen binding; IEA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 614 AA; 67747 MW; 839BAF3B8D124F89 CRC64;  
Query Match 25.3%; Score 431.5; DB 2; Length 614;  
Best Local Similarity 32.3%; Pred. No. 6.4e-26;  
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;  
QY 4 PTVKILQSSCDG-GGHPPTTQLCLVSGYTPGTINITWLEDQVMDVLSTASTQGE 62  
Db 250 PNVNFFVPPRDGFGSPAPRKSCLICEATNFTPKITVSWLKDGLVSGFTTDPVTIENK 309  
QY 63 LASTQ-----SELTLSQKHLSDRITYTCOVYQGHFT-EDSTKKCADSNPRGVSAYLSRP 116  
Db 310 GSTPQTYKVIISTLTISEIDMLNVLNYTCRVDRHGLTFLKNVSTCAASPSTDLITFTIPP 369  
QY 117 SPFDLFIKRSPTITCLVVDLAPSKGTVNLTWSRASKPVNHSRKEEKQKNGTLTSTL 176  
Db 370 SFADIFLSKSNLTCLVSNLAYE-TLNIWSASQSGEPLTKIKIMESHNPCTFSAGVA 428  
QY 177 PVGTRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYATP--EWPGRDRKRT 234  
Db 429 SVCVEDMNNRKEFVCTVTHRLDLPSPQKKFISKPNVHKHPVAVYLLPPAREQLNRESAT 488



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QY 235 LACLIQNFMPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 232
Db 489 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 548
QY 293 DEFICRAVHEAASPSQTVQRAV 314
Db 549 ETYTCVVSHEAL-PHLVTERTV 569

RESULT 10
MUCM MOUSE
ID _MUCM_MOUSE STANDARD; PRT; 475 AA.
AC P01873;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81076590; PubMed=6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RL comparison with other immunoglobulin heavy chain genes.";
RN Nucleic Acids Res. 8:3933-3945(1980).
[2]
RP NUCLEOTIDE SEQUENCE OF 432-475.
RX MEDLINE=80222874; PubMed=6771020; DOI=10.1016/0092-8674(80)90617-0;
RA Early P., Rogers J., Davis M., Calame K., Bond M., Wall R., Hood L.;
RT "Two mRNAs can be produced from a single immunoglobulin mu gene by
RL alternative RNA processing pathways.";
RN Cell 20:313-319(1980).
[3]
RP NUCLEOTIDE SEQUENCE OF 409-475 (MYELOMA MOPC 104E).
RX MEDLINE=80222873; PubMed=6771019; DOI=10.1016/0092-8674(80)90616-9;
RA Rogers J., Early P., Carter C., Calame K., Bond M., Hood L., Wall R.;
RT "Two mRNAs with different 3' ends encode membrane-bound and secreted
RL forms of immunoglobulin mu chain.";
RN Cell 20:303-312(1980).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Membrane-bound;
CC IsoId=P01873-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01872-1; Sequence=External;
CC -1- MISCELLANEOUS: The sequence of residues 1-409 is assumed to be
CC identical with the corresponding region of the secreted form.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00443; AB59651.1; -; Genomic DNA.
CC EMBL; J00444; AB59651.1; JOINED; Genomic_DNA.
CC EMBL; V00821; CAA24202.1; -; mRNA.
CC PIR; A02167; MHMSM.
CC HSSP; P01861; IADQ.
CC GO; GO:0019815; C:B cell receptor complex; IDA.
CC GO; GO:0009897; C:external side of plasma membrane; IDA.
CC GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
CC GO; GO:0048471; C:perinuclear region; IDA.
CC GO; GO:0003623; F:antigen binding; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0004988; F:transmembrane receptor activity; IDA.
CC GO; GO:0000187; P:activation of MAPK; IDA.

QY 293 DEFICRAVHEAASPSQTVQRAV 314
Db 410 ETYTCVVGHEAL-PHLVTERTV 430

RESULT 11
Q8VCX7_MOUSE
ID Q8VCX7_MOUSE PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;

QY 293 DEFICRAVHEAASPSQTVQRAV 314
Db 410 ETYTCVVGHEAL-PHLVTERTV 430

Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKIQSCDG-GGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVLDLSTASTQEGE 62
Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

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Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

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Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

Query Match 25.2%; Score 430.5; DB 1; Length 475;
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Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
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QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
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QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
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QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
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QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
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Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKIQSCDG-GGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVLDLSTASTQEGE 62
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
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Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKIQSCDG-GGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVLDLSTASTQEGE 62
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QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
Db 350 VTCLVGKFSADISVQWLQKQLPQEKYVTSAPMPGAPGYFTHSILTVTEEWNSG 409

Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;

QY 4 PTVKIQSCDG-GGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVLDLSTASTQEGE 62
Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNRKEFCVCTVTRDLPSQPKKFIKPNVHVHKKHPAVYLLPPAREQLNRESAT 349
QY 235 LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRTKSGS-GF-FVFSRLVETRAEWEQK 292
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Query Match 25.2%; Score 430.5; DB 1; Length 475;
Best Local Similarity 32.3%; Pred. No. 5.5e-26;
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QY 4 PTVKIQSCDG-GGHFPPTIQLCLVSGYTGTTNITWLEDQVMDVLDLSTASTQEGE 62
Db 111 PNVNVPVPRDGFSGPAPRKSCLICEATNFTPKPITVSWLKDKGLVESGFTTDPVTIENK 170
QY 63 LASTQ-----SELTLSQKHWLSDRTVTYTCOVTVQGHTEF-EDSTKCKADSNPRGVSALSRP 116
Db 171 GSTPQTYKVISTLTISEIDWLNINVTYCDVHRGLTFLKNVSVSTCAASPTDILTFTIPP 230
QY 117 SPFDLPIRKSPTITCLVVDLAPSKGTNLTWSRASKGPNVHSTRKEEKORNGTLTVTSTL 176
Db 231 SPADIFLSKSNITCLVSNLATYE-TLNISSWASQSGEPLKIKIMESHHPNGTFSAGVA 289
QY 177 PVGTRDWISGETYQCVKRVTHPHLPRLMRSTTTKTSGRAPAEVYVAFATP--EWPGRDKRT 234
Db 290 SVCVEDNNR
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OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2464031;  
RA Sikder S.K., Borden P., Gruzo F., Akolkar P.N., Bhattacharya S.B.,  
RA Morrison S.L., Kabat E.A.;  
RT "Amino acid substitutions in VH CDR2 change the idiotype but not the  
antigen-binding of monoclonal antibodies to alpha(1----6)dextran.";  
RL J. Immunol. 142:888-893(1989).  
DR EMBL; BC018315; AAH18315.1; -; mRNA.  
DR PIR; C30562; C30562.  
DR HSSP; P01751; IAGW.  
DR Ensembl; ENSMUSG00000054328; Mus musculus.  
DR MG1; MG1:96448; Igh-6.  
DR GO; GO:0019815; C:B cell receptor complex; IDA.  
DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
DR GO; GO:0048471; C:perinuclear region; IDA.  
DR GO; GO:0003823; F:antigen binding; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0004888; F:transmembrane receptor activity; IDA.  
DR GO; GO:0000187; P:activation of MAPK activity; IDA.  
DR GO; GO:0003033; P:antigen processing; IDA.  
DR GO; GO:0005853; P:B cell receptor signaling pathway; IDA.  
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.  
DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.  
DR GO; GO:0004807; P:positive regulation of endocytosis; IDA.  
DR GO; GO:0050731; P:positive regulation of peptidyl-tyrosine ph. . .; IDA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 5.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DDA4C22862 CRC64;

Query Match 25.2%; Score 430.5; DB 2; Length 613;  
Best Local Similarity 32.3%; Pred. No. 7.6e-26;  
Matches 104; Conservative 56; Mismatches 149; Indels 13; Gaps 8;  
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DB 249 PNVNVFVPRDGFSGPAPRKSLICEATNFTPKPTVSWLQKGLVSGFTTDPVTIENK 308  
QY 63 LASTQ-----SELTLSQKHWSLDRYTCQVYQCHTF-EDSTKKCADSNPRGVSAIYLSRP 116  
DB 309 GSTPTQYKVVSTITISIDWNLNLYTCRVDRHGLTFLKNVSSCAASPSDILTFTIPP 368  
QY 117 SPFDLFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTKKEQRNGTUTVTSTL 176  
DB 369 SPADIFLKSANLTCLVSNLATVE-TLNIWSQSGSPLETKIKIMESHNPNGTFSAKGVA 427  
QY 177 PVGTRDWIEGTQCRVTHPHLPALMRSTTKTSGPRAAEVYAFATP--EWPGRDCKRT 234  
DB 428 SVCVEDWNNRKEFVCTVTHRDLPSPQKFKISKPNVHKHPVAVYLLPAREQLNRESAT 487  
QY 235 LACLIQNFMPEDISVQWLHNEVQLPDRHSTTOPRTKGS-GF-FVFSRLVETVRAEWQK 292  
DB 488 VTLVGKGFSPADISVQWLQGLLPQKQYVTSAPMPPEFGAFYFTHSILLTVTEENSG 547  
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DB 548 ETVTCVVGHEAL-PHLVTERTV 568  
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AC Q504M7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
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RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
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RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RG NIH MGC Project;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC094936; AAH94936.1; -; mRNA.  
DR InterPro; IPR003599; IG.



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FT REGION 219 324 CH3.
FT REGION 325 454 CH4.
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FT CARBOHYD 112 112 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 192 192 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 210 210 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 238 238 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 257 257 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 280 280 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 441 441 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 13 13 Interchain (with light chain) (Probable).
FT DISULFID 27 88 By similarity.
FT DISULFID 135 198 By similarity.
FT DISULFID 215 215 Interchain (with heavy chain) (Probable).
FT DISULFID 245 304 By similarity.
FT DISULFID 292 292 Interchain (with heavy chain) (Probable).
FT DISULFID 352 414 By similarity.
FT DISULFID 453 453 Interchain (with heavy chain) (Probable).
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SQ SEQUENCE 454 AA; 50197 MW; 4D2134612BE1469 CRC64;

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Best Local Similarity 31.5%; Pred. No. 1.9e-25;
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DB 111 PNVSVFVPSDAFSGPAPKRSRLCEASNFSPKQITVSWLRDGRPKVSGFTTEFVTPEDR 170
QY 63 LASTQ-----SELTLSQKHLSDRYTCQVYQGHTR-EDSTKKCADSNRGSAYLSRP 116
DB 171 GSGRTYKIVSTLTITSEDLNLNLSVYTCVRDHRGLTFWKNSSVCSAASPSTIDIAFPPIP 230
QY 117 SPFDLIRKSPITITCLVVDLAPSKGTNLTWSRSGKPVNHSRTRKEQRNGTLTITVSTL 176
DB 231 SFVGIFLKSATLTLCLVTNLA-TYDTLNISSRSRSGEPLTKTLTESHNGTFSAGEA 289
QY 177 PVGRTRDWEGETYQCRVTHPHLPRALMRSTTKTSOPR-----AAPVYAFATPEWPGSRDK 232
DB 290 NVCVEDMDSGKEFVCTVTHRLPSQPKFISK---PREMNKTPPAVY-----QQPLAREQ 341
QY 233 -----RTLACLIONFPEDISVQWLHNEVOLPDARHSTTOPRKTGSG--FFVFSRLEV 284
DB 342 LILRESATVTCVLVKGFSADIPVQMLQSQPLSQDKYVTSAPMPQPAPHLYFTHSVLTV 401
QY 285 TRAEWEQKDEFCICRAVHEAASPSQTVQRAVSVNPGK 320
DB 402 TEEWNSGETYTCVVGHEAL-PHMVTERTVDRSTGK 436
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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6P6C4; 20-465.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IG1; 3.
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DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
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QY 56 STTGEGELASTQSELTLSQKHLSDRYTCQVYQ-GHTPEDST---KKCADSNP----- 106
DB 194 AVLQSSGLYSLSVYTPVPSNF-GTQVYTCNVDRHKPSNTKYDKTVERKCCVECPCPAPP 252
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DB 253 VAGPSVFLFPKPKDITLMSITPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTPREE 312
QY 165 QRNGLTITVTSTPLVGRDWEGETYQCRVTHPHLPRALMRSTTKTSPPRAAPEVYAFATP 224
DB 313 QFNSTFRVSVLTVVHQDMLNGKEYCKVSKNGLPAPIEKTISKTKGQPREQVYTL--- 369
QY 225 EWPGSRDKRT-----LACLIONFPEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVF 279
DB 370 --PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYNTTTPMILDSGSGFFLY 425
QY 280 SRLVETRAEWQKDEFCICRAVHEAASPSQTVQRAVSVNPGK 320
DB 426 SKLTVDKSRWQQGNVFCSCVMHEALHNHYT-QKSLSLSPGK 465
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Search completed: November 30, 2005, 00:56:33  
Job time : 178.232 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2005, 00:51:35 : Search time 38.2609 Seconds  
(without alignments)  
691.469 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPSQTVQRAVSVNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5 COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCRTUS COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	331	2	US-09-401-636-1
2	1701	99.6	325	2	US-09-701-623C-1
3	1158	67.8	222	2	US-10-211-948-2
4	1146	67.1	222	2	US-10-211-948-8
5	1038.5	60.8	342	2	US-09-401-636-8
6	956.5	56.0	426	1	US-08-336-583-2
7	956.5	56.0	426	4	PCT-US95-13795-2
8	949.5	55.6	431	2	US-09-479-614-14
9	949.5	55.6	496	2	US-09-479-614-2
10	949.5	55.6	496	2	US-09-479-614-29
11	895.5	52.5	312	2	US-09-701-623C-2
12	827	48.4	341	2	US-09-401-636-11
13	793	46.5	340	2	US-09-401-636-2
14	783	45.9	313	2	US-09-701-623C-3
15	781	45.8	341	2	US-09-401-636-3
16	770	45.1	345	2	US-09-401-636-10
17	751	44.0	341	2	US-09-401-636-9
18	745	43.6	341	2	US-09-401-636-4
19	744	43.6	504	2	US-09-091-645C-2
20	744	43.6	676	2	US-09-091-645C-4
21	720	42.2	341	2	US-09-401-636-6
22	716.5	42.0	342	2	US-09-401-636-5
23	709.5	41.6	343	2	US-09-401-636-7
24	691.5	40.5	313	2	US-09-701-623C-4
25	678.5	39.7	561	2	US-09-192-545-2
26	597	35.0	113	1	US-08-232-539D-56
27	587	34.4	110	1	US-08-399-108A-6

28	587	34.4	110	1	US-08-433-105A-6	Sequence 6, Appli
29	587	34.4	110	1	US-08-434-869A-6	Sequence 6, Appli
30	581	34.0	109	1	US-08-037-579A-2	Sequence 2, Appli
31	581	34.0	109	2	US-08-601-184-2	Sequence 2, Appli
32	566.5	33.2	109	2	US-08-466-163B-1	Sequence 1, Appli
33	566.5	33.2	109	2	US-09-802-096-1	Sequence 1, Appli
34	566.5	33.2	109	2	US-09-802-077-1	Sequence 1, Appli
35	566.5	33.2	109	2	US-09-925-179-1	Sequence 1, Appli
36	556	32.6	106	1	US-08-232-539D-54	Sequence 54, Appli
37	526	30.8	119	1	US-08-464-025A-1	Sequence 1, Appli
38	508.5	29.8	118	2	US-08-466-151-1	Sequence 1, Appli
39	481.5	28.2	334	1	US-08-646-981-16	Sequence 17, Appli
40	480.5	28.1	474	2	US-09-828-995B-17	Sequence 16, Appli
41	477.5	28.0	352	2	US-09-828-995B-38	Sequence 38, Appli
42	476.5	27.9	375	2	US-09-828-995B-32	Sequence 32, Appli
43	476.5	27.9	473	2	US-09-828-995B-20	Sequence 20, Appli
44	472.5	27.7	470	2	US-09-828-995B-11	Sequence 11, Appli
45	468.5	27.4	468	2	US-09-828-995B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-401-636-1  
; Sequence 1, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401.636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq For Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-1

Query Match	100.0%;	Score 1707;	DB 2;	Length 331;
Best Local Similarity	100.0%;	Pred. No. 3.3e-156;	Mismatches 0;	Indels 0; Gaps 0;
Matches 320;	Conservative 0;			
Qy	1	FTPTVKILQSSCDGGGHPPTIQLCLVSGYTGCTINITWLEDQVMDVLDLSTASTTQE	60	
Db	12	FTPTVKILQSSCDGGGHPPTIQLCLVSGYTGCTINITWLEDQVMDVLDLSTASTTQE	71	
Qy	61	GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRSPFD	120	
Db	72	GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRSPFD	131	
Qy	121	LFIRKSPITICLVLDLAPSKGTVALTWSRASKPVNHSTRKEEKORNGTLTVTSTLPVGT	180	
Db	132	LFIRKSPITICLVLDLAPSKGTVALTWSRASKPVNHSTRKEEKORNGTLTVTSTLPVGT	191	
Qy	181	RDWTEGYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ	240	
Db	192	RDWTEGYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ	251	
Qy	241	NFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFFVFSRLVETRAEWEQKDEFCRAV	300	
Db	252	NFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFFVFSRLVETRAEWEQKDEFCRAV	311	
Qy	301	HEAASPSQTVQRAVSVNPGK	320	
Db	312	HEAASPSQTVQRAVSVNPGK	331	

RESULT 2  
US-09-701-623C-1  
; Sequence 1, Application US/09701623C  
; Patent No. 6811782  
; GENERAL INFORMATION:  
; APPLICANT: Wang Ph.D., Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY  
; FILE REFERENCE: 11514153US1  
; CURRENT APPLICATION NUMBER: US/09/701.623C  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: CH2CH3 of human IgE  
; PUBLICATION INFORMATION:  
; AUTHORS: Dorrington,  
; JOURNAL: Immunology  
; VOLUME: 41  
; PAGES: 3-25  
; DATE: 1978  
US-09-701-623C-1  
Query Match 99.6%; Score 1701; DB 2; Length 325;  
Best Local Similarity 99.4%; Pred. No. 1.2e-155;  
Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 FTPTVKILSSCDGGHFPPTQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 60  
Db 6 FTPTVKILSSCDGGHFPPTQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 65  
Qy 61 GELASTOSELTLSQKWLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 120  
Db 66 GELASTOSELTLSQKWLSDRTYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 125  
Qy 121 LFIKSPITICLVVDLAPSKGTVNLWTSRASKGKPVNHSRKEKQKNGTLTVTSTLPVGT 180  
Db 126 LFIKSPITICLVVDLAPSKGTVNLWTSRASKGKPVNHSRKEKQKNGTLTVTSTLPVGT 185  
Qy 181 RDWIEGTQYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
Db 186 RDWIEGTQYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245  
Qy 241 NMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVTAEWEQKDEFICRAV 300  
Db 246 NMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVSRLEVTAEWEQKDEFICRAV 305  
Qy 301 HEAAASPSQTQVRAVSNVPGK 320  
Db 306 HEAAASPSQTQVRAVSNVPGK 325  
RESULT 3  
US-10-211-948-2  
; Sequence 2, Application US/10211948  
; Patent No. 6889145  
; GENERAL INFORMATION:  
; APPLICANT: Jardtetzky, Theodore S.  
; APPLICANT: Wurzburg, Beth A.  
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A Fc REGION OF AN IGE ANTIBODY AND USE THEREOF  
; FILE REFERENCE: AL-9-C3  
; CURRENT APPLICATION NUMBER: US/10/211,948

; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: 09/809,746  
; PRIOR FILING DATE: 2001-03-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-211-948-2  
Query Match 67.8%; Score 1158; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 1.6e-103; Indels 0; Gaps 0;  
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 103 DSNPRGVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGKPVNHSRKE 162  
Db 5 DSNPRGVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGKPVNHSRKE 64  
Qy 163 EKORNGTLTVTSTLPVGTDRDIEGTQYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAF 222  
Db 65 EKORNGTLTVTSTLPVGTDRDIEGTQYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAF 124  
Qy 223 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 282  
Db 125 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 184  
Qy 283 EVTRAWEQKDEFICRAVHEAASPSQTQVRAVSNVPGK 320  
Db 185 EVTRAWEQKDEFICRAVHEAASPSQTQVRAVSNVPGK 222  
RESULT 4  
US-10-211-948-8  
; Sequence 8, Application US/10211948  
; Patent No. 6889145  
; GENERAL INFORMATION:  
; APPLICANT: Jardtetzky, Theodore S.  
; APPLICANT: Wurzburg, Beth A.  
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A Fc REGION OF AN IGE ANTIBODY AND USE THEREOF  
; FILE REFERENCE: AL-9-C3  
; CURRENT APPLICATION NUMBER: US/10/211,948  
; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: 09/809,746  
; PRIOR FILING DATE: 2001-03-15  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 222  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-211-948-8  
Query Match 67.1%; Score 1146; DB 2; Length 222;  
Best Local Similarity 99.1%; Pred. No. 2.3e-102; Indels 0; Gaps 0;  
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 103 DSNPRGVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGKPVNHSRKE 162  
Db 5 DSNPRGVSAYLSRSPFDLFIKSPITICLVVDLAPSKGTVNLWTSRASKGKPVNHSRKE 64  
Qy 163 EKORNGTLTVTSTLPVGTDRDIEGTQYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAF 222  
Db 65 EKORNGTLTVTSTLPVGTDRDIEGTQYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAF 124  
Qy 223 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 282  
Db 125 TPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTOPRKTGSGFFVFSRL 184  
Qy 283 EVTRAWEQKDEFICRAVHEAASPSQTQVRAVSNVPGK 320  
Db 185 EVTRAWEQKDEFICRAVHEAASPSQTQVRAVSNVPGK 222

RESULT 5  
US-09-401-636-8  
; Sequence 8, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401.636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-8

Query Match 60.8%; Score 1038.5; DB 2; Length 342;  
Best Local Similarity 62.4%; Pred. No. 9.9e-92;  
Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;  
QY 3 PPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQ 60  
DB 22 PPTVKILPHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVWLVLDGQEAENLFPYTPRKREG 81  
QY 61 GELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPPD 120  
DB 82 GOTFLQSEVNITQGMWSSNTYTHVKNHSIPEDSSRKCCADSNPRGVSAYLSRPSPPD 141  
QY 121 LPIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEKQKNGTLTSTLPGVT 180  
DB 142 LPIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEKQKNGTLTSTLPGVT 201  
QY 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAF-ATPEWPGSRDKRTLACL 239  
DB 202 RDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPPEETGT--TRIVTCL 259  
QY 240 QNFMPEDISQVWLHNEVQLPDARHSTTQPRKTGKS--GFFVFSRLEVTRAWEQKDFIC 297  
DB 260 RGFYEPSEISQVWLHNEEDHTGHTTTRPQKHGTDPSFFLYSRMLVNKSIWEKGNLVT 319  
QY 298 RAVHEAASPSQTVQRAVSNPG 319  
DB 320 RVVHEALPGSRRTLEKSLHYSAG 341

RESULT 6  
US-08-336-583-2  
; Sequence 2, Application US/08336583  
; Patent No. 5629415  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,583  
FILING DATE: 09-NOV-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 19211  
TELEPHONE: (908) 594-6734  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 426 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-583-2

Query Match 56.0%; Score 956.5; DB 1; Length 426;  
Best Local Similarity 56.2%; Pred. No. 1.1e-83;  
Matches 182; Conservative 50; Mismatches 87; Indels 5; Gaps 4;  
QY 1 FTPPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59  
DB 104 FIPTVKILPHSSCDPNVGDTHITQLLCLISGYVGDMEVWLVDGQKATNIFPYTAPGCK 163  
QY 60 EGELASTQSELTLSQKHWLSDRTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPF 119  
DB 164 EGNVTSTHSELNITQGEWVSQKTYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPL 223  
QY 120 DLPIKSPITICLVVDLAPSKGTNLTWSRASKPVNHSRKEKQKNGTLTSTLPGV 179  
DB 224 DLYVHKAPKICLVVDLAPSKGTNLTWSRASKPVNHSRKEKQKNGTLTSTLPGV 282  
QY 180 TRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-ENWPGSRDKRTLACL 238  
DB 283 TNDWIEGETYQCRVTHPHLPRALMRSTTKLPGKRLAPEVYMLPPSPPEETGT--TRIVTCL 342  
QY 239 IQNFMPEDISQVWLHNEVQLPDARHSTTQPRKTGKS--GFFVFSRLEVTRAWEQKDFI 296  
DB 343 IQNFMPEDISQVWLHNEEDHTGHTTTRPQKHGTDPSFFLYSRMLVNKSIWEKGNLVT 402  
QY 297 RAVHEAASPSQTVQRAVSNPGK 320  
DB 403 QVVVHEALSGSRILQKRWVSKTPGK 426

RESULT 7  
PCT-US95-13795-2  
; Sequence 2, Application PC/TUS9513795  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; APPLICATION NUMBER: PCT/US95/13795  
; FILING DATE:

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;
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 56.08; Score 956.5; DB 4; Length 426;
Best Local Similarity 56.2%; Pred. No. 1.1e-83;
Matches 182; Conservative 50; Mismatches 87; Indels 5; Gaps 4;

Qy 1 FTPTVKILQSSCDGGHFPPTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 59
Db 104 FIPTVKLFHSSCNPLGDTGTTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 163
Qy 60 EGELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPF 119
Db 164 EGNVTSHSELNITQGEWVSQKTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPL 223
Qy 120 DLFRKSPPTITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVG 179
Db 224 DLYVHKAPKTCVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVN 282
Qy 180 TRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 238
Db 283 TNDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 342
Qy 239 IQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 296
Db 343 IQNFFPADISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 402
Qy 297 CRVHEAASPQTVORAVSNPGK 320
Db 403 CQVVHEALSGSRILQKWSKTPGK 426

RESULT 8
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 55.6%; Score 949.5; DB 2; Length 431;
Best Local Similarity 56.5%; Pred. No. 5.3e-83;
Matches 183; Conservative 46; Mismatches 90; Indels 5; Gaps 4;

Qy 1 FTPTVKILQSSCDGGHFPPTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 59
Db 174 FIPTVKLFHSSCNPLGDTGTTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 233
Qy 60 EGELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPF 119
Db 234 EGNVTSHSELNITQGEWVSQKTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPL 293
Qy 120 DLFRKSPPTITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVG 179
Db 294 DLYVHKSPKITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVD 352
Qy 180 TRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 238
Db 353 ATDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 412
Qy 239 IQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 296
Db 413 IQNFFPPDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 472
Qy 297 CRVHEAASPQTVORAVSNPGK 320
Db 473 CQVVHEALPGFRTLKKSVMKNGPK 496
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Db 109 FIPTVKLFHSSCNPLGDTGTTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 168
Qy 60 EGELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPF 119
Db 169 EGNVTSHSELNITQGEWVSQKTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPL 228
Qy 120 DLFRKSPPTITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVG 179
Db 229 DLYVHKSPKITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVD 287
Qy 180 TRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 238
Db 288 ATDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 347
Qy 239 IQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 296
Db 348 IQNFFPPDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 407
Qy 297 CRVHEAASPQTVORAVSNPGK 320
Db 408 CQVVHEALPGFRTLKKSVMKNGPK 431

RESULT 9
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 55.6%; Score 949.5; DB 2; Length 496;
Best Local Similarity 56.5%; Pred. No. 6.5e-83;
Matches 183; Conservative 46; Mismatches 90; Indels 5; Gaps 4;

Qy 1 FTPTVKILQSSCDGGHFPPTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 59
Db 174 FIPTVKLFHSSCNPLGDTGTTIQLCLISGVYVPGDMEVTLVLDGQKATNIFPYTAPGK 233
Qy 60 EGELASTQSELTSQKHWLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPF 119
Db 234 EGNVTSHSELNITQGEWVSQKTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRPSPL 293
Qy 120 DLFRKSPPTITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVG 179
Db 294 DLYVHKSPKITCLVVDLAPSKGTNLTWSRAGSKPVNHSRKEEKQKNGTLTWTSTLPVD 352
Qy 180 TRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 238
Db 353 ATDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTIACL 412
Qy 239 IQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 296
Db 413 IQNFFPPDISVQWLHNEVOLPDARHSTTQPRKTKG--SGFFVFSRLVETRAEWQKDEFI 472
Qy 297 CRVHEAASPQTVORAVSNPGK 320
Db 473 CQVVHEALPGFRTLKKSVMKNGPK 496
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RESULT 10
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 55.6%; Score 949.5; DB 2; Length 496;
Best Local Similarity 56.5%; Pred. No. 6.5e-83;
Matches 183; Conservative 46; Mismatches 90; Indels 5; Gaps 4;

Qy 1 FPPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
Db 174 FIPPTVKLFHSSCNPLDGTGTIQLCLISGVPGDMETWLVGQKATNIPPTAPGKQ 233
Qy 60 EGELASTQSELTLSQKHLSDRYTCQVYQGHTEFEDSTKCKADSNPRGVSAYLSRSPF 119
Db 234 EKVSTHSELNITQGEVWSQKTYTCQVYQGFEDHARKTESDPFGVSYLSPSPPL 293
Qy 120 DLFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSTRKEEKQKRGNTLTVTSTLPVG 179
Db 294 DLVYHKSPKITCLVVDLANTDGM-LTWSRENGESVHPDPMVKTKYNGTITVTSTLPVD 352
Qy 180 TRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEW-PGSRDKRTLA 238
Db 353 ATDWIEGETYQCKVTHPLPKDIVRSIAKAPGRFPPEVYVFLPPEGEPKTKDKVILTCL 412
Qy 239 IQNMPEDISVQWLHNEVQLPDARHSTTOPRKTG--SGFFVFSRLEVTAEWEQKDEFI 296
Db 413 IQNFPFPPDISVQWLHNDSPVTEQQTATWPHKATGSPAFFVFSRLEVSRLADWEQORDVFT 472
Qy 297 CRAVHEAASPSQTVQRAVSNPGK 320
Db 473 CQVHEALPGFRTLKKSYSKNPGK 496

RESULT 11
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF ALLERGY
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IgE
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; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match 52.5%; Score 895.5; DB 2; Length 312;
Best Local Similarity 55.1%; Pred. No. 5.3e-78;
Matches 172; Conservative 48; Mismatches 83; Indels 9; Gaps 5;

Qy 1 FPPPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQ-VMDVDLSTASTTQ 59
Db 6 FIPPTVKLFHSSCNPNVGDTHTTIQLCLISGVPGDMETWLVGQKATNIPPTAPGK 65
Qy 60 EGELASTQSELTLSQKHLSDRYTCQVYQGHTEFEDSTKCKADSNPRGVSAYLSRSPF 119
Db 66 EGNVTSTHSELNITQGEVWSQKTYTC---QGFTFKDEARKCESDPFGVSYLSPSPPL 121
Qy 120 DLFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSTRKEEKQKRGNTLTVTSTLPVG 179
Db 122 DLVYHKAPKITCLVVDLATMEG-MNLTWYRESKEPVNPGPLNKKDHFNIGTITVTSTLPVN 180
Qy 180 TRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATP-EMPGRDKRTLA 238
Db 181 TNDWIEGETYQCRVTHPHLPKDIVRSIAKAPGRAPDVLFLPPEBEQGTQKDRVTLTCL 240
Qy 239 IQNMPEDISVQWLHNEVQLPDARHSTTOPRKTG--GFFVFSRLEVTAEWEQKDEFI 296
Db 241 IQNFPFPPDISVQWLHNDSPITQDQYTTGPHKVSGRPAFFIFSRLEVSRLVDSQKQKFT 300
Qy 297 CRAVHEAASPSQ 308
Db 301 CQVHEALSGSR 312

RESULT 12
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-11

Query Match 48.4%; Score 827; DB 2; Length 341;
Best Local Similarity 49.7%; Pred. No. 2.4e-71;
Matches 160; Conservative 58; Mismatches 96; Indels 8; Gaps 5;

Qy 3 PPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQ 60
Db 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVTVLVDVQGAENLFPVTPPKREG 81
Qy 61 EGELASTQSELTLSQKHLSDRYTCQVYQGHTEFEDSTKCKADSNPRGVSAYLSRSPF 120
Db 82 GQTFSLQSEVNITQQQWMSNTYTVCHVXNGSIFEDSSRKCESDPFGVSYLSPSPPL 141
Qy 121 LFIKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSTRKEEKQKRGNTLTVTSTLPVGT 180
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Db 142 LYVHKAPKITCLVVDLATMEG-MNLTWYRESKPEVNPGLNKKDKHFNFGTITVTSTLPVNT 200  
Qy 181 RDMIEGTYOCRVTHPLPALMRSTTKTSPRAAPEVYAF-ATPEWPGSRDKRTIACLI 239  
Db 201 NDWIEGTYOCRVTHPLPKDVRSAIAKPKGLAPEVYMLPPSPBETGT--TRTVTCLI 258  
Qy 240 QNFPEPDISVQWLHNEVQLPDARHSTTQPRKTGSG--GFFVFGRLVETRAEWQKQDFIC 297  
Db 259 RGFVPSISVQWLHNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNKSINWKGMLVTC 318  
Qy 298 RAVHEAASPSQTVQRAVSVNPG 319  
Db 319 RVVHEALPGSRTLEKSLHYSAG 340

RESULT 13

US-09-401-636-2  
; Sequence 2, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401.636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-2

Query Match 46.5%; Score 793; DB 2; Length 340;  
Best Local Similarity 47.4%; Pred. No. 4.6e-69;  
Matches 152; Conservative 54; Mismatches 109; Indels 6; Gaps 5;

Qy 2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTQOE 60  
Db 12 TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHIQNDVSIHMLMDRDKIYETHAQNVLIKEE 70  
Qy 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120  
Db 71 GKLASTYSRLNITQQQWSESTFTCKVTSGENYWAHTRRCSDDPRGVITYLIPSPDL 130  
Qy 121 LFRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTWTSTLPVGT 180  
Db 131 LYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSASQSRSTKHNNATTSITSLPVD 189  
Qy 181 RDMIEGTYOCRVTHPLPALMRSTTKTSPRAAPEVYAFATPEWPGSRDKRTIACLIQ 240  
Db 190 KMWIEGTYOCRVDPHPPFKPIVRSITKALGSAPEVYVFLPPE-EEKDKKTLTCLIQ 248  
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSG--FFVFSRLVETRAEWQKQDFIC 298  
Db 249 NFFPEDISVQWLQDSKLIPKSQHSSTTTPKYNQSNORFFIFSRLEVTKALWTQTKQFTCR 308  
Qy 299 AVHEAASPSQTVQRAVSVNPG 319  
Db 309 VIHEALREPKRLERTISKSLG 329

RESULT 14

US-09-701-623C-3  
; Sequence 3, Application US/09701623C  
; Patent No. 6811782  
; GENERAL INFORMATION:  
; APPLICANT: Wang Ph.D., Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

; TITLE OF INVENTION: ALLERGY  
; FILE REFERENCE: 11514153U1  
; CURRENT APPLICATION NUMBER: US/09/701.623C  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: RAT  
; FEATURE:  
; OTHER INFORMATION: CH2CH3 of rat Ige  
; PUBLICATION INFORMATION:  
; AUTHORS: Dorrington,  
; AUTHORS: Bennich,  
; JOURNAL: Immunology  
; VOLUME: 41  
; PAGES: 3-25  
; DATE: 1978  
; PUBLICATION INFORMATION:  
; AUTHORS: Patel,  
; JOURNAL: Immunogenetics  
; VOLUME: 41  
; PAGES: 282-286  
; DATE: 1995  
; PUBLICATION INFORMATION:  
; AUTHORS: Steen,  
; JOURNAL: J. Mol. Biol.  
; VOLUME: 177  
; PAGES: 19-32  
; DATE: 1984  
; PUBLICATION INFORMATION:  
; AUTHORS: Ishida,  
; JOURNAL: EMBO J.  
; VOLUME: 1  
; PAGES: 1117-1123  
; DATE: 1982  
US-09-701-623C-3

Query Match 45.9%; Score 783; DB 2; Length 313;  
Best Local Similarity 49.2%; Pred. No. 3.8e-67;  
Matches 150; Conservative 49; Mismatches 100; Indels 6; Gaps 5;

Qy 2 TPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWL-EDGQVMDVDLSTASTQOE 60  
Db 7 TKPTVDLLHSSCDPNA-FHSTIQLYCFVYGHIQNDVSIHMLMDRDKIYETHAQNVLIKEE 65  
Qy 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD 120  
Db 66 GKLASTYSRLNITQQQWSESTFTCKVTSGENYWAHTRRCSDDPRGVITYLIPSPDL 125  
Qy 121 LFRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTWTSTLPVGT 180  
Db 126 LYENGTPKLTCLVLDL-ESEENITVTWVRERKKSIGSASQSRSTKHNNATTSITSLPVD 184  
Qy 181 RDMIEGTYOCRVTHPLPALMRSTTKTSPRAAPEVYAFATPEWPGSRDKRTIACLIQ 240  
Db 185 KMWIEGTYOCRVDPHPPFKPIVRSITKALGSAPEVYVFLPPE-EEKDKKTLTCLIQ 243  
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSG--FFVFSRLVETRAEWQKQDFIC 298  
Db 244 NFFPEDISVQWLQDSKLIPKSQHSSTTTPKYNQSNORFFIFSRLEVTKALWTQTKQFTCR 303  
Qy 299 AVHEA 303  
Db 304 VIHEA 308

RESULT 15

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US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match          45.8%; Score 781; DB 2; Length 341;
Best Local Similarity 47.8%; Pred. No. 6.6e-67;
Matches 154; Conservative 59; Mismatches 101; Indels 8; Gaps 5;

Qy 3 PPTVKILOSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDGQVMD--VDLSTASTTQE 60
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVITWLDGQAEANLFPYTRPKREG 81
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Qy 61 GELASTQSELTLISQKHWLSDRITYTCQVTYQGHTPEDSTKCADSNPRGVSAYLSRPSPPD 120
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 82 GQTFSLQSEVNITQQWMSNTYTCHVKXNGSIFEDSAQKSDTDPRGISAYILPPTPQD 141
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Qy 121 LFIKSPRTITCLVVDLAPSKGTVNLTWGRAGKPVNHSRKEEKQKRNGLTIVTSTLPVGT 180
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 142 LFKVKVPTIGCLIVDLA-SAENVKVTWSRGSGPVNPSLVVKEQYNGTFTVTSHPVNT 200
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Qy 181 RDWIEGETYQCRVTHPHLPRLMRSTTKTSGPRAAPEVYAP-ATPEWPGSRDKRTLACLI 239
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 201 DDWIEGDTYTCRLSPDMPVPLIRTISKAPGKRLAPEVYMLPPSPPEETGT--TRTVTCLI 258
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Qy 240 QNFMPEDISVQWLHNEVQLPDAHSTTTPRKTKGS--GFFVFSRLVTRAEWEQKDEFIC 297
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 259 RGFPSEISVQWLFNNEEDHTGHHTTTRPKDHDGTDPSFFLYSRMLVNKSIWEKGNLVTC 318
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Qy 298 RAVHEAASPSTQVQRAVSNPG 319
    |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 319 RVVHEALPGSRTLKSLHYSAG 340
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Job time : 39.2609 secs

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:56:45 ; Search time 133.913 Seconds  
(without alignments)  
998.449 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPSQTVQRAVSNVPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.Main.\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	1707	100.0	320	3	US-09-847-208-6	Sequence 6, Appli
2	1707	100.0	320	4	US-10-000-439-6	Sequence 6, Appli
3	1707	100.0	323	3	US-09-949-375A-2	Sequence 2, Appli
4	1707	100.0	323	3	US-09-949-375A-4	Sequence 4, Appli
5	1707	100.0	323	3	US-09-949-375A-6	Sequence 6, Appli
6	1707	100.0	323	4	US-10-363-954A-2	Sequence 2, Appli
7	1707	100.0	323	4	US-10-363-954A-4	Sequence 4, Appli
8	1707	100.0	323	4	US-10-363-954A-6	Sequence 6, Appli
9	1707	100.0	327	5	US-10-627-556-224	Sequence 224, App
10	1707	100.0	331	3	US-09-401-636-1	Sequence 1, Appli
11	1707	100.0	331	4	US-10-176-664-1	Sequence 1, Appli
12	1707	100.0	331	4	US-10-207-655-329	Sequence 329, App
13	1707	100.0	331	4	US-10-673-594-1	Sequence 1, Appli
14	1707	100.0	331	5	US-10-627-556-97	Sequence 97, Appli
15	1707	100.0	331	5	US-10-627-556-174	Sequence 174, App
16	1707	100.0	427	3	US-09-847-208-5	Sequence 5, Appli
17	1707	100.0	427	4	US-10-000-439-5	Sequence 5, Appli
18	1707	100.0	428	3	US-09-916-230-1	Sequence 1, Appli
19	1707	100.0	428	3	US-09-949-375A-1	Sequence 1, Appli
20	1707	100.0	428	4	US-10-047-542-60	Sequence 60, Appli
21	1707	100.0	428	4	US-10-363-954A-1	Sequence 1, Appli
22	1707	100.0	569	3	US-09-847-208-7	Sequence 7, Appli
23	1707	100.0	569	4	US-10-000-439-7	Sequence 7, Appli
24	1707	100.0	574	4	US-10-047-542-45	Sequence 45, Appli
25	1707	100.0	574	4	US-10-214-524-37	Sequence 37, Appli
26	1707	100.0	574	4	US-10-050-902-176	Sequence 176, App
27	1707	100.0	574	4	US-10-050-898-176	Sequence 176, App

ALIGNMENTS

RESULT 1

US-09-847-208-6

; Sequence 6, Application US/09847208

; Publication No. US20030082190A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; APPLICANT: Zhang, Ke

; APPLICANT: Zhu, Daocheng

; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES

; FILE REFERENCE: UC67.002A

; CURRENT APPLICATION NUMBER: US/09/847.208

; CURRENT FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 320

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-847-208-6

Query Match 100.0%; Score 1707; DB 3; Length 320;  
Best Local Similarity 100.0%; Pred. No. 2.4e-127; Mismatches 0; Indels 0; Gaps 0;  
Matches 320; Conservative 0;

Qy	1	FTPTVKILQSSCDGGGHPPTIQLCLIVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE	60
Db	1	FTPTVKILQSSCDGGGHPPTIQLCLIVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE	60
Qy	61	GELASTQSELTSQKHWLSDRITYTCQVTYQHTFEDSTKGCADSNPRGVAYLSRPSPPD	120
Db	61	GELASTQSELTSQKHWLSDRITYTCQVTYQHTFEDSTKGCADSNPRGVAYLSRPSPPD	120
Qy	121	LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPNVHSTRKEEKORNGTLTWTSTLPVGT	180
Db	121	LFIRKSPITICLVVDLAPSKGTVNLWTSRASKPNVHSTRKEEKORNGTLTWTSTLPVGT	180
Qy	181	RDWTEGETYQCRVTHPHLPRALMESTTKTSGPRAAPEVYAFATPEWPGSRDKRTIACLIQ	240
Db	181	RDWTEGETYQCRVTHPHLPRALMESTTKTSGPRAAPEVYAFATPEWPGSRDKRTIACLIQ	240
Qy	241	NFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFFVFSRLVETRAWEQKDEFICRAV	300
Db	241	NFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFFVFSRLVETRAWEQKDEFICRAV	300
Qy	301	HEAASPSQTVQRAVSNVPGK 320	
Db	301	HEAASPSQTVQRAVSNVPGK 320	

Sequence 384, App  
Sequence 334, App  
Sequence 129, App  
Sequence 248, App  
Sequence 176, App  
Sequence 180, App  
Sequence 184, App  
Sequence 8, Appli  
Sequence 7, Appli  
Sequence 35, Appli  
Sequence 34, Appli  
Sequence 34, Appli  
Sequence 10, Appli  
Sequence 10, Appli  
Sequence 13, Appli  
Sequence 26, Appli

```
RESULT 2
US-10-000-439-6
; Sequence 6, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-6

Query Match      100.0%; Score 1707; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60
Db 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60
QY 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 120
QY 121 LFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db 121 LFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
QY 181 RDWIEGTYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 181 RDWIEGTYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
QY 241 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 241 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
QY 301 HEAASPSTQVQRAVSVNPGK 320
Db 301 HEAASPSTQVQRAVSVNPGK 320

RESULT 3
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human IgE heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)

; OTHER INFORMATION: Human IgE heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human IgE heavy chain C4 domain
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (196)..(206)
; OTHER INFORMATION: Epitope in FG loop
US-09-949-375A-2

Query Match      100.0%; Score 1707; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 60
Db 4 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLBGQVMDVLDLSTASTTQE 63
QY 61 GELASTQSELTLSQKHLSDRTYTCQVYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 120
Db 64 GELASTQSELTLSQKHLSDRTYTCQVYQGHTFEDSTKKCADSNPRGVSAYLSRSPFD 123
QY 121 LFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db 124 LFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 183
QY 181 RDWIEGTYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 184 RDWIEGTYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243
QY 241 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 300
Db 244 NFMPEDISVQWLHNEVQLDPARHSTTQPRKTGSGFFVFSRLEVTAEWEQKDEFICRAV 303
QY 301 HEAASPSTQVQRAVSVNPGK 320
Db 304 HEAASPSTQVQRAVSVNPGK 323

RESULT 4
US-09-949-375A-4
; Sequence 4, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
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; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.
US-09-949-375A-4

Query Match      100.0%; Score 1707; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
Db 4 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 63
Qy 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPPD 120
Db 64 GELASTQSELTLSQKHWSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPPD 123
Qy 121 LPIKSPITICLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180
Db 124 LPIKSPITICLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLTVTSTLPVGT 183
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 184 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243
Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFCICRAV 300
Db 244 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFCICRAV 303
Qy 301 HEAASPSQTVQRAVSNVPGK 320
Db 304 HEAASPSQTVQRAVSNVPGK 323

RESULT 5
US-09-949-375A-6
; Sequence 6, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.
US-09-949-375A-6

Query Match      100.0%; Score 1707; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 60
Db 4 FTPTVKILQSSCDGGHPPPTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTTQE 63
Qy 61 GELASTQSELTLSQKHWSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPPD 120
Db 64 GELASTQSELTLSQKHWSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAYLSRPSPPD 123
Qy 121 LPIKSPITICLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180

; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human Ige heavy chain C2 domain
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)
; OTHER INFORMATION: Human Ige heavy chain C3 domain
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human Ige heavy chain C4 domain
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; NAME/KEY: MISC FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; NAME/KEY: MISC FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:

; DB 124 LPIKSPITICLVVDLAPSKGTVNLTWRSRSGKPVNHSRKEEKQKNGTLTVTSTLPVGT 183
; Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
; Db 184 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 243
; Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFCICRAV 300
; Db 244 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFCICRAV 303
; Qy 301 HEAASPSQTVQRAVSNVPGK 320
; Db 304 HEAASPSQTVQRAVSNVPGK 323

RESULT 6
US-10-363-954A-2
; Sequence 2, Application US/10363954A
; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; CURRENT FILING DATE: 2003-03-06
; PRIOR FILING DATE: 2003-03-06
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human Ige heavy chain C2 domain
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)
; OTHER INFORMATION: Human Ige heavy chain C3 domain
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human Ige heavy chain C4 domain
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; NAME/KEY: MISC FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; NAME/KEY: MISC FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
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;	NAME/KEY:	MISC FEATURE	
	LOCATION:	(196)..(206)	
	OTHER INFORMATION:	Epitope in FG loop	
	US-10-363-954A-2		
Query Match 100.0%; Score 1707; DB 4; Length 323;			
Best Local Similarity 100.0%; Pred. No. 2.4e-127;			
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	FTPTVKILQSSCDGGGHPPTIQLCLVSGYPTGTTINITWLEDGQVMDVLDLSTASTTQE	60
Db	4	FTPTVKILQSSCDGGGHPPTIQLCLVSGYPTGTTINITWLEDGQVMDVLDLSTASTTQE	63
Qy	61	GELASTQSELTLSQKHWSLDRVTTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD	120
Db	64	GELASTQSELTLSQKHWSLDRVTTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD	123
Qy	121	LFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQNGTLTSTLPLVGT	180
Db	124	LFIRKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKQNGTLTSTLPLVGT	183
Qy	181	RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLQ	240
Db	184	RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLQ	243
Qy	241	NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV	300
Db	244	NFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQKDEFICRAV	303
Qy	301	HEAASPSQTVQRAVSNPGK 320	
Db	304	HEAASPSQTVQRAVSNPGK 323	
RESULT 7			
US-10-363-954A-4			
; Sequence 4, Application US/10363954A			
; Publication No. US20040156838A1			
; GENERAL INFORMATION:			
; APPLICANT: KLYSNER, Steen et al.			
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE			
; FILE REFERENCE: 4614-0115P			
; CURRENT APPLICATION NUMBER: US 60/232,831			
; PRIOR FILING DATE: 2003-03-06			
; PRIOR APPLICATION NUMBER: US/10/363,954A			
; CURRENT FILING DATE: 2000-09-15			
; PRIOR APPLICATION NUMBER: US 60/232,831			
; PRIOR FILING DATE: 2000-09-15			
; PRIOR APPLICATION NUMBER: DK PA 2000 01326			
; PRIOR FILING DATE: 2000-09-06			
; NUMBER OF SEQ ID NOS: 38			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 323			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Artificial protein sequence optimized for expression in mammalian			
; OTHER INFORMATION: cells of human IgE heavy chain fragment spanning C2, C3, and C4.			
; OTHER INFORMATION: Human IgE heavy chain C1 domain			
; NAME/KEY: DOMAIN			
; LOCATION: (11)..(116)			
; OTHER INFORMATION: Human IgE heavy chain C1 domain			
US-10-363-954A-4			
Query Match 100.0%; Score 1707; DB 4; Length 323;			
Best Local Similarity 100.0%; Pred. No. 2.4e-127;			
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	FTPTVKILQSSCDGGGHPPTIQLCLVSGYPTGTTINITWLEDGQVMDVLDLSTASTTQE	60
Db	4	FTPTVKILQSSCDGGGHPPTIQLCLVSGYPTGTTINITWLEDGQVMDVLDLSTASTTQE	63
Qy	61	GELASTQSELTLSQKHWSLDRVTTCQVYQGHTEFEDSTKKCADSNPRGVSAYLSRSPFD	120



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RESULT 9
US-10-627-556-224
; Sequence 224, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 224
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-10-627-556-224

Query Match 100.0%; Score 1707; DB 5; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVLDLSTASTTQE 60
Db 8 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVLDLSTASTTQE 67

Qy 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 120
Db 68 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 127

Qy 121 LFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTSTLPVGT 180
Db 128 LFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTSTLPVGT 187

Qy 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 188 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 300
Db 248 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 307

Qy 301 HEAASPSQTQVRAVSNPGK 320
Db 308 HEAASPSQTQVRAVSNPGK 327

RESULT 10
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1

Query Match 100.0%; Score 1707; DB 3; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVLDLSTASTTQE 60
Db 12 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVLDLSTASTTQE 71

Qy 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 120
Db 72 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 131

Qy 121 LFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTSTLPVGT 180
Db 132 LFIKSPITICLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQKNGTLTSTLPVGT 191

Qy 181 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 192 RDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 251

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 300
Db 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAWEQKDEFICRAV 311

Qy 301 HEAASPSQTQVRAVSNPGK 320
Db 312 HEAASPSQTQVRAVSNPGK 331

RESULT 11
US-10-176-664-1
; Sequence 1, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-1

Query Match 100.0%; Score 1707; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVLDLSTASTTQE 60
Db 12 FTPTVKILQSSCDGGGHPPTIQLCLVSGVTGCTINITWLEDQVMDVLDLSTASTTQE 71

Qy 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFSTKCCADSNPRGVSAYLSRPSFD 120
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Db 72 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 131

Qy 121 LFRKSPPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEKQKNGTLTVTSTLTPVGT 180

Db 132 LFRKSPPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEKQKNGTLTVTSTLTPVGT 191

Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKETLACLIQ 240

Db 192 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKETLACLIQ 251

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 300

Db 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 311

Qy 301 HEAASPSQTVQRAVSNPGK 320

Db 312 HEAASPSQTVQRAVSNPGK 331

RESULT 12

US-10-207-655-329

Query Match 100.0%; Score 1707; DB 4; Length 331;

Best Local Similarity 100.0%; Pred. No. 2.5e-127;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.

TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS

FILE REFERENCE: 390069.401C1

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SOFTWARE: PatentIn version 3.0

SEQ ID NO 329

TYPE: PRT

LENGTH: 331

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: fusion polypeptide

US-10-207-655-329

Query Match 100.0%; Score 1707; DB 4; Length 331;

Best Local Similarity 100.0%; Pred. No. 2.5e-127;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60

Db 8 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 67

Qy 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120

Db 68 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 127

Qy 121 LFRKSPPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEKQKNGTLTVTSTLTPVGT 180

Db 128 LFRKSPPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEKQKNGTLTVTSTLTPVGT 187

Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKETLACLIQ 240

Db 188 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKETLACLIQ 247

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 300

Db 248 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 307

Qy 301 HEAASPSQTVQRAVSNPGK 320

Db 308 HEAASPSQTVQRAVSNPGK 327

RESULT 13

US-10-673-594-1

Query Match 100.0%; Score 1707; DB 4; Length 331;

Best Local Similarity 100.0%; Pred. No. 2.5e-127;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/10/673,594

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 331

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically generated proteins

US-10-673-594-1

Query Match 100.0%; Score 1707; DB 4; Length 331;

Best Local Similarity 100.0%; Pred. No. 2.5e-127;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 60

Db 12 FTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE 71

Qy 61 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 120

Db 72 GELASTQSELTLSQKHWLSDRITYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD 131

Qy 121 LFRKSPPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEKQKNGTLTVTSTLTPVGT 180

Db 132 LFRKSPPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRTRKEKQKNGTLTVTSTLTPVGT 191

Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKETLACLIQ 240

Db 192 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVAFATPEWPGSRDKETLACLIQ 251

Qy 241 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 300

Db 252 NFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLEVTAEWEQKDEFICRAV 311

Qy 301 HEAASPSQTVQRAVSNPGK 320

Db 312 HEAASPSQTVQRAVSNPGK 331

RESULT 14

US-10-627-556-97

Query Match 100.0%; Score 1707; DB 4; Length 331;

Best Local Similarity 100.0%; Pred. No. 2.5e-127;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Ledbetter, Jeffrey A.

TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

FILE REFERENCE: 49076.000004.CIP2

CURRENT APPLICATION NUMBER: US/10/627,556

CURRENT FILING DATE: 2003-07-26

PRIOR APPLICATION NUMBER: 10/053,530

PRIOR FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: 60/367,358

PRIOR FILING DATE: 2002-01-16

PRIOR APPLICATION NUMBER: 09/765,208

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/385,691

PRIOR FILING DATE: 2002-06-03

NUMBER OF SEQ ID NOS: 699

SOFTWARE: PatentIn version 3.2

SEQ ID NO 97

LENGTH: 331

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-556-97

Query Match      100.0%; Score 1707; DB 5; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEDQVMDVLDLSTASTQOE 60
Db 8 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEDQVMDVLDLSTASTQOE 67

Qy 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFDSYKCCADSNPRGVSAYLSRPSFFD 120
Db 68 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFDSYKCCADSNPRGVSAYLSRPSFFD 127

Qy 121 LFIKSPITITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQKRNGLTIVTSTLPVGT 180
Db 128 LFIKSPITITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQKRNGLTIVTSTLPVGT 187

Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240
Db 188 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 247

Qy 241 NFWPEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLEVTRAWEQKDEFICRAV 300
Db 248 NFWPEDISVQWLHNEVOLPDARHSTTOPRKTGSGFFVFSRLEVTRAWEQKDEFICRAV 307

Qy 301 HEAASPSQTVQRAVSVNPGK 320
Db 308 HEAASPSQTVQRAVSVNPGK 327

Search completed: November 30, 2005, 01:16:49
Job time : 134.913 secs
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RESULT 15
US-10-627-556-174
; Sequence 174, Application US/10627556
; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.CIP2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-556-174

Query Match      100.0%; Score 1707; DB 5; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.5e-127;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEDQVMDVLDLSTASTQOE 60
Db 8 FTPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTINITWLEDQVMDVLDLSTASTQOE 67

Qy 61 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFDSYKCCADSNPRGVSAYLSRPSFFD 120
Db 68 GELASTQSELTLSQKHWSLSDRTYTCQVYQGHTEFDSYKCCADSNPRGVSAYLSRPSFFD 127
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2005, 01:10:40 ; Search time 6.37681 Seconds  
(without alignments)  
152.100 Million cell updates/sec

Title: US-09-847-208B-6

Perfect score: 1707

Sequence: 1 FTPTVKILQSSCDGGGHP.....HEAASPQTQVRASVNVNPGK 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
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- 6: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1701	99.6	US-10-723-207-1	Sequence 1, Appli
2	895.5	52.5	US-10-723-207-2	Sequence 2, Appli
3	783	45.9	US-10-723-207-3	Sequence 3, Appli
4	691.5	40.5	US-10-723-207-4	Sequence 4, Appli
5	425	24.9	US-11-144-248-45	Sequence 45, Appl
6	425	24.9	US-11-144-248-46	Sequence 46, Appl
7	425	24.9	US-11-144-248-49	Sequence 49, Appl
8	425	24.9	US-11-144-248-50	Sequence 50, Appl
9	422	24.7	US-11-025-712-12	Sequence 12, Appl
10	419	24.5	US-11-022-289-6	Sequence 6, Appli
11	416	24.4	US-11-144-248-28	Sequence 28, Appl
12	416	24.4	US-11-022-289-7	Sequence 7, Appli
13	416	24.4	US-11-022-289-8	Sequence 8, Appli
14	414.5	24.3	US-11-022-289-3	Sequence 3, Appli
15	414	24.3	US-10-723-207-40	Sequence 40, Appl
16	414	24.3	US-11-022-289-2	Sequence 2, Appli
17	413	24.2	US-11-022-289-4	Sequence 4, Appli
18	413	24.2	US-11-022-289-5	Sequence 5, Appli
19	399	23.4	US-11-172-320-6	Sequence 6, Appli
20	397.5	23.3	US-11-022-289-11	Sequence 11, Appl
21	397	23.3	US-11-174-186-41	Sequence 41, Appl
22	394.5	23.1	US-11-022-289-1	Sequence 1, Appli
23	394.5	23.1	US-11-022-289-10	Sequence 10, Appl
24	394	23.1	US-10-723-207-31	Sequence 31, Appl
25	376.5	22.1	US-11-016-503-10	Sequence 10, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-723-207-1

; Sequence 1, Application US/10723207

; Publication No. US20050250934A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; APPLICANT: Walfield, Alan M.

; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

; TITLE OF INVENTION: ALLERGY

; FILE REFERENCE: 1151-4153052

; CURRENT APPLICATION NUMBER: US/10/723,207

; CURRENT FILING DATE: 2003-11-24

; PRIOR FILING DATE: 09/701,623

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; PRIOR FILING DATE: 1998-06-20

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 325

; TYPE: PRT

; ORGANISM: HUMAN

; FEATURE:

; OTHER INFORMATION: CH2CH3 of human Ige

; PUBLICATION INFORMATION:

; AUTHORS: Dorrington,

; AUTHORS: Bennich,

; JOURNAL: Immunology

; VOLUME: 41

; PAGES: 3-25

; DATE: 1978

US-10-723-207-1

Query Match

Best Local Similarity 99.4%; Score 1701; DB 1; Length 325;

Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTATTQE 60

Db 6 FTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVLDLSTATTQE 65

Qy 61 GELASTQSELTLSQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPSPD 120

Db 66 GELASTQSELTLSQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPSPD 125

Qy 121 LFIKSPITITCLVLDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTSTLPVGT 180

Sequence 6, Appli  
Sequence 8, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 16, Appli  
Sequence 12, Appli  
Sequence 14, Appli  
Sequence 17, Appli  
Sequence 390, App  
Sequence 11, Appli  
Sequence 2, Appli  
Sequence 389, App  
Sequence 14, Appli  
Sequence 18, Appli  
Sequence 9, Appli  
Sequence 30, Appli  
Sequence 4, Appli  
Sequence 20, Appli  
Sequence 22, Appli  
Sequence 16, Appli

Db 126 LFIKSGPTTICLVVDLAPSGTWNLTWSRAGKPVNHSRKKEQRNGTLTSTLPVGT 185  
Qy 181 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 240  
Db 186 RDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQ 245  
Qy 241 NFWPDISVQWLHNEVOLPARHSTTQPRKTKSGGFFVFSRLRVTRAWEQKDEFTICRAV 300  
Db 246 NFWPDISVQWLHNEVOLPARHSTTQPRKTKSGGFFVFSRLRVTRAWEQKDEFTICRAV 305  
Qy 301 HEAASPSQTVORAVSNPGK 320  
Db 306 HEAASPSQTVORAVSNPGK 325  
RESULT 2  
US-10-723-207-2  
; Sequence 2, Application US/10723207  
; Publication No. US20050250934A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; FILE REFERENCE: 1151-4153US2  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Dog  
; FEATURE:  
; OTHER INFORMATION: CH2CH3n of dog IGE  
; PUBLICATION INFORMATION:  
; AUTHORS: Patel,  
; JOURNAL: Immunogenetics  
; VOLUME: 41  
; PAGES: 282-286  
; DATE: 1995  
US-10-723-207-2  
Query Match 52.5%; Score 895.5; DB 1; Length 312;  
Best Local Similarity 55.1%; Pred. No. 5.2e-56;  
Matches 172; Conservative 48; Mismatches 83; Indels 9; Gaps 5;  
Qy 1 FPTPTVKILOSSCDGGGHFPPTTOLLCLVSGYTPGTINITWLEDGQ-VMDVDLSTATTQ 59  
Db 6 FIPPTVKLFHSSCNFVGDTHTTIOLLCLISGYVPGDMEVILWLDGQKATNIFYTAPGTK 65  
Qy 60 EGEASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKTKCADSNPRGVSAYLSRSPFF 119  
Db 66 EGNVTSTHSELNITQQGWSQKTYTC---QGFTFKDEARKKCSDEPRGVTISLSPSPSL 121  
Qy 120 DLFIKSGPTTICLVVDLAPSGTWNLTWSRAGKPVNHSRKKEQRNGTLTSTLPVGT 179  
Db 122 DLYVHKAPKICTLVLDLATWEG-MNLTWYRESKEPVNPGPLNKKOHFNHITVTSTLPVN 180  
Qy 180 TRDWIEGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATP-EWPGSRDKRTLACLI 238  
Db 181 TNDWIEGETYQCRVTHPHLPKDIIVRSIAKAPGKRAPPDVYLFPLPPEEQGTOKDRTVLTCL 240  
Qy 239 IQNFWPDISVQWLHNEVOLPARHSTTQPRKTKGS--GFFVFSRLRVTRAWEQKDEFTI 296  
Db 241 IQNFWPDISVQWLHNEVOLPARHSTTQPRKTKGS--GFFVFSRLRVTRAWEQKDEFTI 300

Qy 297 CRAVHEAASPSQ 308  
Db 301 CQWHEALSGSR 312  
RESULT 3  
US-10-723-207-3  
; Sequence 3, Application US/10723207  
; Publication No. US20050250934A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; FILE REFERENCE: 1151-4153US2  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 313  
; TYPE: PRT  
; ORGANISM: RAT  
; FEATURE:  
; OTHER INFORMATION: CH2CH3 of rat IGE  
; PUBLICATION INFORMATION:  
; AUTHORS: Dorrington,  
; JOURNAL: Immunology  
; VOLUME: 41  
; PAGES: 3-25  
; DATE: 1978  
; PUBLICATION INFORMATION:  
; AUTHORS: Patel,  
; JOURNAL: Immunogenetics  
; VOLUME: 41  
; PAGES: 282-286  
; DATE: 1995  
; PUBLICATION INFORMATION:  
; AUTHORS: Steen,  
; JOURNAL: J. Mol. Biol.  
; VOLUME: 177  
; PAGES: 19-32  
; DATE: 1984  
; PUBLICATION INFORMATION:  
; AUTHORS: Ishida,  
; JOURNAL: EMBO J.  
; VOLUME: 1  
; PAGES: 1117-1123  
; DATE: 1982  
US-10-723-207-3  
Query Match 45.9%; Score 783; DB 1; Length 313;  
Best Local Similarity 49.2%; Pred. No. 3.1e-48;  
Matches 150; Conservative 49; Mismatches 100; Indels 6; Gaps 5;  
Qy 2 TPPTVKILOSSCDGGGHFPPTIQLCLVSGYTPGTINITWL-EDGQVMDVDLSTATTQ 60  
Db 7 TRPTVDLLHSSCDPNA-FHSTIQLCYCFVYGHQNDVSIHLMDDRKIYDTHAQNVLIKEE 65  
Qy 61 GEIASTQSELTLSQKHLSDRTYTCQVYQGHFTFEDSTKTKCADSNPRGVSAYLSRSPFF 120  
Db 66 GKLAITYSRNITQQQWMESEFTCKTSQGENYWAHTRCSDDEPRGVITYLIPSPSLD 125  
Qy 121 LFIKSGPTTICLVVDLAPSGTWNLTWSRAGKPVNHSRKKEQRNGTLTSTLPVGT 180

Db 126 LYENGTPKLTCLVLDL-ESEENITVWVRERKKSIGSASORSTKHNATTSTISILPVD 184  
 Qy 181 RDWIEGTYQCRVTHPLPALMSTTKTSFRAAPEVAFATPEWPGSRDKRTCLAQ 240  
 Db 185 KDWIEGTYQCRVTHPLPALMSTTKTSFRAAPEVAFATPEWPGSRDKRTCLAQ 243  
 Qy 241 NFMPEIDISVQWLHNEVQLPDARHSTTPQRTKSGS--FFVFSRLVTRAEWEQDEFICR 298  
 Db 244 NFFEDISVQWLHNEVQLPDARHSTTPQRTKSGS--FFVFSRLVTRAEWEQDEFICR 303  
 Qy 299 AVHEA 303  
 Db 304 VIHEA 308

RESULT 4  
 US-10-723-207-4  
 ; Sequence 4, Application US/10723207  
 ; Publication No. US20050250934A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Chang Yi  
 ; APPLICANT: Walfield, Alan M.  
 ; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
 ; TITLE OF INVENTION: ALLERGY  
 ; FILE REFERENCE: 1151-4153US2  
 ; CURRENT APPLICATION NUMBER: US/10/723,207  
 ; CURRENT FILING DATE: 2003-11-24  
 ; PRIOR APPLICATION NUMBER: 09/701,623  
 ; PRIOR FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/US99/13959  
 ; PRIOR FILING DATE: 1999-06-21  
 ; PRIOR APPLICATION NUMBER: 09/100,287  
 ; PRIOR FILING DATE: 1998-06-20  
 ; NUMBER OF SEQ ID NOS: 91  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 313  
 ; TYPE: PRT  
 ; ORGANISM: MOUSE  
 ; FEATURE:  
 ; OTHER INFORMATION: CH2CH3 of mouse Ige  
 US-10-723-207-4

Query Match 40.5%; Score 691.5; DB 1; Length 313;  
 Best Local Similarity 46.4%; Pred. No. 6.3e-42;  
 Matches 136; Conservative 51; Mismatches 101; Indels 5; Gaps 5;  
 Qy 13 CDGGHFPPTIQLCLVSGYTPGTITNITWL-EDGQVMDVLDSTASTOGEELASTQSELT 71  
 Db 19 CDPNA-FHSTIQLYCFIYGHILNDVSVWLMDDREITDTLAQTVLKKEGKLASTCSKLN 77  
 Qy 72 LSQKHLSDRTYTCQVYQGHTEFSDTKKCADSNPRGVSAYLSRSPFDFLRKSPPTIC 131  
 Db 78 ITEQWMSESTTCRVTSQGCYLAHTRCPDHEPRGATYLIPLPSPLDLYQNGAPKLT 137  
 Qy 132 LVVDLAPSKGTNLTWSRAGKPVNHSRKEKQNGILTVSTLPGTRDWIEGETYQC 191  
 Db 138 LVVDLESEK-NVNVITWNOEKTSVSASOWYTKHNNATTSITSLPVAKWIEGYGYQC 196  
 Qy 192 RVTHPLPALMRSTTKTSFRAAPEVAFATPEWPGSRDKRTCLAQNFPMPEISVQW 251  
 Db 197 IVDRPDPFKPIVRSITKTPQRSAPVYVFPPEE-ESEDKKTLTCLQNFPPEDISVQW 255  
 Qy 252 LHNEVQLPDARHSTTPQRTKGS-GFFVFSRLVTRAEWEQDEFICRAVHEA 303  
 Db 256 LGDGKLSNSQHSSTTPLKSNQNGQFFIFSRLEVAKTLWTQKQTCQVIEHA 308

RESULT 5  
 US-11-144-248-45  
 ; Sequence 45, Application US/11144248  
 ; Publication No. US2005024408A1  
 ; GENERAL INFORMATION:

; APPLICANT: Cohen, Bruce D.  
 ; APPLICANT: Beebe, Jean  
 ; APPLICANT: Miller, Penelope E.  
 ; APPLICANT: Moyer, James D.  
 ; APPLICANT: Corvalan, Jose R.  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
 ; FILE REFERENCE: ABX-PF2  
 ; CURRENT APPLICATION NUMBER: US/11/144,248  
 ; CURRENT FILING DATE: 2005-06-02  
 ; PRIOR APPLICATION NUMBER: US/10/038,591  
 ; PRIOR FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: 60/259,927  
 ; PRIOR FILING DATE: 2001-01-05  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 45  
 ; LENGTH: 470  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-11-144-248-45

Query Match 24.9%; Score 425; DB 7; Length 470;  
 Best Local Similarity 31.3%; Pred. No. 2.3e-23;  
 Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;  
 Qy 5 TVKILQSSCDGGHFP-----PTIQLCLVSGYTPGTITNITWLEDGQVMDVLDST 54  
 Db 139 TVTSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFFPEPVTWS-NSGALTSGVHTF 197  
 Qy 55 ASTTQEGELASTQSELTLSQRHLSDRITYTCQVYQ-GHTFEDST---KKCADSNP---- 106  
 Db 198 PAVLQSSGLYSLSSVTVTPSSNF-GTQYTCNVDPKPSNTKVDKTVKCKCCVECPCPAP 256  
 Qy 107 --RGVSAYLSRSPFD-LFIRKSPITCLVDLAPSKGTNLTWSRAGKPVNHSRKEE 163  
 Db 257 PVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNMYVDGVEVHNATKPRE 316  
 Qy 164 KORNGTLTVTSTPLVGTTRDWIEGTYQCRVTHPLPALMRSTTKTSFRAAPEVAFAT 223  
 Db 317 EQFNSTFRVSVLTVVHODWLNQKEYCKVSNKGLPAPIEKTIISKTQGPQVYTL-- 374  
 Qy 224 PEWPGSRDKRT-----LACLQNFMPEDISVQWLHNEVQLPDARHSTTPQRTKSGGFFV 278  
 Db 375 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPPMLDSGSPFL 429  
 Qy 279 FSRLEVTRAEWEQDEFICRAVHEAASPSQTVQRAVSNPGK 320  
 Db 430 YSKLTVDKSRWQGNVFCVSMHEALHNHYT-QKSLSLSPGK 470

RESULT 6  
 US-11-144-248-46  
 ; Sequence 46, Application US/11144248  
 ; Publication No. US2005024408A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Bruce D.  
 ; APPLICANT: Beebe, Jean  
 ; APPLICANT: Miller, Penelope E.  
 ; APPLICANT: Moyer, James D.  
 ; APPLICANT: Corvalan, Jose R.  
 ; APPLICANT: Gallo, Michael  
 ; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
 ; FILE REFERENCE: ABX-PF2  
 ; CURRENT APPLICATION NUMBER: US/11/144,248  
 ; CURRENT FILING DATE: 2005-06-02  
 ; PRIOR APPLICATION NUMBER: US/10/038,591  
 ; PRIOR FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: 60/259,927  
 ; PRIOR FILING DATE: 2001-01-05  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 46

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; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-46

Query Match      24.9%; Score 425; DB 7; Length 470;
Best Local Similarity 31.3%; Pred. No. 2.3e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;

Qy 5 TVKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDST 54
Db 139 TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTF 197
Qy 55 ASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP---- 106
Db 198 PAVLQSSGLYSLSSVTVPSNFGTQYTCNVDHKPSNTKVDKTVVERKCCVCEPCPCAP 256

Qy 107 --RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEE 163
Db 257 PVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTKPRE 316
Qy 164 KORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT 223
Db 317 EQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTL-- 374
Qy 224 PEWPGSRDKT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
Db 375 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPNENYKTTTPMMLDSGSGFFL 429
Qy 279 FSRLEVTAEWQKDEFCICRAVHEAASPSQTVORAVSVNPGK 320
Db 430 YSKLTVDKSRWQGNVFCSCVMHEALHNHYT--QKSLSLSPGK 470

RESULT 7
US-11-144-248-49
; Sequence 49, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-49

Query Match      24.9%; Score 425; DB 7; Length 470;
Best Local Similarity 31.3%; Pred. No. 2.3e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;

Qy 5 TVKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDST 54
Db 139 TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTF 197
Qy 55 ASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP---- 106
Db 198 PAVLQSSGLYSLSSVTVPSNFGTQYTCNVDHKPSNTKVDKTVVERKCCVCEPCPCAP 256

Qy 107 --RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEE 163
Db 257 PVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTKPRE 316
Qy 164 KORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT 223
Db 317 EQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTL-- 374
Qy 224 PEWPGSRDKT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
Db 375 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPNENYKTTTPMMLDSGSGFFL 429
Qy 279 FSRLEVTAEWQKDEFCICRAVHEAASPSQTVORAVSVNPGK 320
Db 430 YSKLTVDKSRWQGNVFCSCVMHEALHNHYT--QKSLSLSPGK 470

RESULT 8
US-11-144-248-50
; Sequence 50, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-50

Query Match      24.9%; Score 425; DB 7; Length 473;
Best Local Similarity 31.3%; Pred. No. 2.4e-23;
Matches 107; Conservative 60; Mismatches 139; Indels 36; Gaps 11;

Qy 5 TVKILQSSCDGGGHP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDST 54
Db 142 TVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW-NSGALTSGVHTF 200
Qy 55 ASTTQEGELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP---- 106
Db 201 PAVLQSSGLYSLSSVTVPSNFGTQYTCNVDHKPSNTKVDKTVVERKCCVCEPCPCAP 259
Qy 107 --RGVSAYLSRSPFD-LFIRKSPITICLVVDLAPSKGTVNLTWSRASGKPVNHSRKEE 163
Db 260 PVAGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNKTKPRE 319
Qy 164 KORNGTLTVTSTLPVGTTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFAT 223
Db 320 EQFNSTFRVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTL-- 377
Qy 224 PEWPGSRDKT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFV 278
Db 378 ---PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPNENYKTTTPMMLDSGSGFFL 432
Qy 279 FSRLEVTAEWQKDEFCICRAVHEAASPSQTVORAVSVNPGK 320
Db 433 YSKLTVDKSRWQGNVFCSCVMHEALHNHYT--QKSLSLSPGK 473
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RESULT 9
US-11-025-712-12
; Sequence 12, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
;           Thomas, G. Roger
;           Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/025,712
; FILING DATE: 28-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/404,286
; FILING DATE: 31-Mar-2003
; APPLICATION NUMBER: 09/811384
; FILING DATE: 20-Dec-2000
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-Feb-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-Jan-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, David W.
; REGISTRATION NUMBER: NONE
; REFERENCE/DOCKET NUMBER: P1729C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1739
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-025-712-12
Query Match 24.7%; Score 422; DB 7; Length 450;
Best Local Similarity 31.1%; Pred. No. 3.6e-23;
Matches 106; Conservative 61; Mismatches 138; Indels 36; Gaps 11;
QY 6 VKILOSCDGGHFP-----PTIQLCLVSGYPTGTINITWLEDGQVMDVLDSTA 55
DB 120 VTVSGASTKPSVFPFLAPCSRSTSESTAALGLVKDYFPPEPTVSN-NSGALTSGVHTFP 178
QY 56 SITQEGELASTQSELTLSQKHWLSORTYTCQVYQ-GHTFEDST---KKCADSNP----- 106
DB 179 AVLQSGSLSLSVVTVTSNFGTQYTCNVDPKPSNTKVDKTKVERKCCVCPCPAPP 237
QY 107 -RGVSAYLSRSPFD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEEK 164
DB 238 VAGPSVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYDGMVHNKTKPREE 297
QY 165 QRNGTLTVTSTLPVGRDMIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATP 224
DB 298 QFNSTFRVSVLTVVHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL--- 354
QY 225 EWPGRDCKT-----LACLIQNFMPEDISVQWLHNEVQLPDARHSITQPRKTKGSGFFVFP 279

RESULT 10
US-11-022-289-6
; Sequence 6, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 195831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-6
Query Match 24.5%; Score 419; DB 7; Length 557;
Best Local Similarity 30.2%; Pred. No. 7.2e-23;
Matches 100; Conservative 57; Mismatches 136; Indels 38; Gaps 9;
QY 20 PPT-----IQLCLVSGYPTGTINITWLEDGQVMDVLDSTASTQEGELASTQSELT 71
DB 235 PPSRDELTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT 294
QY 72 LSQKHWLSDRYTCQVYQG-HTF-----EDSTKKCADSNP-----RGVSAYLSR 115
DB 295 VDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPKDKTHTCPPAPALGQPSVFLFP 354
QY 116 PSPFD-LFIRKSPITICLVLDLAPSKGTVNLTSRASGKPVNHSRKEEKQKNGTLTVTS 174
DB 355 PKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGMVHNKTKPREEQYNSTVTVVS 414
QY 175 TLPVGRDMIEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPFWPGSRDKKT 234
DB 415 VLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSRDEL 469
QY 235 -----LACLIQNFMPEDISVQWLHNEVQLPDARHSITQPRKTKGSGFFVFSRLEVTRAEW 289
DB 470 KNQVSLTCLVKGFYPSDIAVEWESN--GQPNENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 527
QY 290 EKQDFICRAVHEAASPSQTQVRAVSNPGK 320
DB 528 QGQNVFCSCVMHEALHNHYT-QKSLSLSPGK 557

RESULT 11
US-11-144-248-28
; Sequence 28, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
```

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; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-28

Query Match      24.4%; Score 416; DB 7; Length 326;
Best Local Similarity 31.2%; Pred. No. 6.8e-23;
Matches 105; Conservative 59; Mismatches 136; Indels 36; Gaps 11;

Qy 11 SSCDGGHFP-----PTIQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOE 60
Db 1 ASTKGSVFPLAPCSRSTSESTAALGCLVXDYFPEPTVSW-NSGALTSGVHTFPAVLQS 59
Qy 61 GELASTQSELTLSQKHWLSDRITYTCQVYQ-GHTFEDST---KKCADSNP-----RGVS 110
Db 60 SGLYSLSSVTVSSNF-GTQYTCNVDHKPSNTKVDKTVVERKCCVECPCPAPPVAGPS 118
Qy 111 AYLSRSPFD-LPIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKORNGT 169
Db 119 VFLFPKPKDTLMSRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNNAKTKPREEQFNST 178
Qy 170 LTVSTLPGVTRDIEGETYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS 229
Db 179 FRVSVLTVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPQVYTL-----PPS 233
Qy 230 RDKRT-----LACLIONFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFRGLEV 284
Db 234 REEMTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPMVLDSGDSFFLYSKLT 291
Qy 285 TRAEWEQKDFICRAVHEAASPSQTQVRAVSNPGK 320
Db 292 DKSRWQOGNVFSCVMHEALHNHYT-QKSLSLSPGK 326

RESULT 12
US-11-022-289-7
; Sequence 7, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-7

Query Match      24.4%; Score 416; DB 7; Length 551;
Best Local Similarity 30.1%; Pred. No. 1.1e-22;
Matches 98; Conservative 58; Mismatches 136; Indels 34; Gaps 8;

Qy 20 PPT-----IQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOGELASTQSELT 71
Db 235 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNQPENNYKTTTPVLDSDGDSFFLYSKLT 294
Qy 72 LSQKHWLSDRITYTCQVYQGHTEPDSSTKKCADSNP-----RGVSAYLSRSPFD 120
Db 295 VDKSRWQOGNVFSCVMHEA-LHNHYTQKSLSPGKPPAPPELLGGPSVFLFPPKPKD 353
Qy 121 -LPIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVG 179
Db 354 TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQNSTYRVVSVLTVL 413
Qy 180 TRDIEGETYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRT----- 234
Db 414 HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSRDELTKNQVS 468
Qy 235 LACLIONFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFRGLEVTRAEWEQKDE 294
Db 469 LTCVLKGFYPSDIAVEWESN--GQPENNYKTTTPVLDSDGDSFFLYSKLTVDKSRWQOGNV 526
Qy 295 FICRAVHEAASPSQTQVRAVSNPGK 320
Db 527 FSCVMHEALHNHYT-QKSLSLSPGK 551

RESULT 13
US-11-022-289-8
; Sequence 8, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-8

Query Match      24.4%; Score 416; DB 7; Length 551;
Best Local Similarity 30.1%; Pred. No. 1.1e-22;
Matches 98; Conservative 58; Mismatches 136; Indels 34; Gaps 8;

Qy 20 PPT-----IQLCLVSGYTPGTINITWLEDGQVMDVLDLSTASTQOGELASTQSELT 71
Db 235 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNQPENNYKTTTPVLDSDGDSFFLYSKLT 294
Qy 72 LSQKHWLSDRITYTCQVYQGHTEPDSSTKKCADSNP-----RGVSAYLSRSPFD 120
Db 295 VDKSRWQOGNVFSCVMHEA-LHNHYTQKSLSPGKPPAPPELLGGPSVFLFPPKPKD 353
Qy 121 -LPIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKORNGTLTVTSTLPVG 179
Db 354 TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQNSTYRVVSVLTVL 413
Qy 180 TRDIEGETYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRT----- 234
Db 414 HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSRDELTKNQVS 468
Qy 235 LACLIONFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFRGLEVTRAEWEQKDE 294
Db 469 LTCVLKGFYPSDIAVEWESN--GQPENNYKTTTPVLDSDGDSFFLYSKLTVDKSRWQOGNV 526
Qy 295 FICRAVHEAASPSQTQVRAVSNPGK 320
Db 527 FSCVMHEALHNHYT-QKSLSLSPGK 551

RESULT 14
US-11-022-289-3
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:33:18 ; Search time 10 Seconds  
(without alignments)  
172.462 Million cell updates/sec

Title: US-09-847-208B-7  
Perfect score: 3060  
Sequence: 1 EPKCDKTHTCPCPAPELL.....HEAASPTQVRAVNVPGK 569

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1701	55.6	325	1 US-10-723-207-1	Sequence 1, Appli
2	1518	49.6	557	7 US-11-022-289-6	Sequence 6, Appli
3	1513	49.4	551	7 US-11-022-289-8	Sequence 8, Appli
4	1513	49.4	557	7 US-11-022-289-4	Sequence 4, Appli
5	1511	49.4	551	7 US-11-022-289-7	Sequence 7, Appli
6	1511	49.4	557	7 US-11-022-289-5	Sequence 5, Appli
7	1510	49.3	557	7 US-11-022-289-2	Sequence 2, Appli
8	1497.5	48.9	548	7 US-11-022-289-3	Sequence 3, Appli
9	1412.5	46.2	564	7 US-11-022-289-10	Sequence 10, Appl
10	1225	40.0	330	7 US-11-022-289-11	Sequence 11, Appl
11	1225	40.0	444	7 US-11-172-320-6	Sequence 6, Appli
12	1225	40.0	452	7 US-11-016-503-6	Sequence 6, Appli
13	1225	40.0	459	1 US-10-949-720-390	Sequence 390, App
14	1225	40.0	462	7 US-11-016-503-8	Sequence 8, Appli
15	1225	40.0	489	1 US-10-835-475-11	Sequence 11, Appl
16	1225	40.0	514	1 US-10-835-475-2	Sequence 2, Appli
17	1225	40.0	557	7 US-11-016-503-4	Sequence 4, Appli
18	1225	40.0	567	7 US-11-016-503-2	Sequence 2, Appli
19	1225	40.0	567	7 US-11-016-503-10	Sequence 10, Appl
20	1225	40.0	771	1 US-10-949-720-389	Sequence 389, App
21	1219	39.8	330	7 US-11-022-289-1	Sequence 1, Appli
22	1219	39.8	579	7 US-11-174-186-41	Sequence 41, Appl
23	1205.5	39.4	531	7 US-11-008-727-18	Sequence 18, Appl
24	1195	39.1	455	7 US-11-016-503-14	Sequence 14, Appl
25	1195	39.1	458	7 US-11-016-503-12	Sequence 12, Appl

26	1195	39.1	458	7 US-11-016-503-16	Sequence 16, Appl
27	1189	38.9	227	7 US-11-008-727-14	Sequence 14, Appl
28	1176	38.4	430	7 US-11-016-503-17	Sequence 17, Appl
29	1107	36.2	326	7 US-11-144-248-28	Sequence 28, Appl
30	1107	36.2	470	7 US-11-144-248-45	Sequence 45, Appl
31	1107	36.2	470	7 US-11-144-248-46	Sequence 46, Appl
32	1107	36.2	470	7 US-11-144-248-49	Sequence 49, Appl
33	1107	36.2	473	7 US-11-144-248-50	Sequence 50, Appl
34	1104	36.1	450	7 US-11-025-712-12	Sequence 12, Appl
35	896.5	29.3	312	1 US-10-723-207-2	Sequence 2, Appli
36	785.5	25.7	476	7 US-11-008-727-22	Sequence 22, Appli
37	784	25.6	313	1 US-10-723-207-3	Sequence 3, Appli
38	779	25.5	509	7 US-11-008-727-16	Sequence 16, Appli
39	776	25.4	236	7 US-11-008-727-4	Sequence 4, Appli
40	776	25.4	470	7 US-11-008-727-20	Sequence 20, Appli
41	693	22.6	313	1 US-10-723-207-4	Sequence 4, Appli
42	414	13.5	76	1 US-10-723-207-40	Sequence 40, Appli
43	394	12.9	76	1 US-10-723-207-31	Sequence 31, Appli
44	334.5	10.9	353	7 US-11-022-289-9	Sequence 9, Appli
45	330	10.8	64	1 US-10-723-207-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1  
US-10-723-207-1  
; Sequence 1, Application US/10723207  
; Publication No. US20050250934A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; APPLICANT: Walfield, Alan M.  
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
; TITLE OF INVENTION: ALLERGY  
; FILE REFERENCE: 1151-4153US2  
; CURRENT APPLICATION NUMBER: US/10/723.207  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: 09/701,623  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: PCT/US99/13959  
; PRIOR FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: 09/100,287  
; PRIOR FILING DATE: 1998-06-20  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: HUMAN  
; FEATURE:  
; OTHER INFORMATION: CH2CH3 of human IGE  
; PUBLICATION INFORMATION:  
; AUTHORS: Dorrington,  
; AUTHORS: Bennich,  
; JOURNAL: Immunology  
; VOLUME: 41  
; PAGES: 3-25  
; DATE: 1978  
US-10-723-207-1

Query Match	55.6%;	Score 1701;	DB 1;	Length 325;
Best Local Similarity	99.4%;	Pred. No. 6.3e-77;		
Matches 318;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
QY	250	FTPTVKILQSSCDGGHFPPTIQLCLVSGVTPGTINITWLEDGQVMDVLDLSTATTQE	309	
Db	6	FTPTVKILQSSCDGGHFPPTIQLCLVSGVTPGTINITWLEDGQVMDVLDLSTATTQE	65	
QY	310	GELASTQSELTLSQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD	369	
Db	66	GELASTQSELTLSQKHLSDRYTCQVYQGHFTFEDSTKCCADSNPRGVSAYLSRSPFD	125	
QY	370	LFIRKSPITCLVVDLAPSKGTVNLTSRASKPVNHSRKEKQNGTLTSTLTPVGT	429	

Db 126 LFIKRSPTITCLVVDLAPSGVTNLTWSRAGKPVNHSIRKEKQKNGTLTVTSTLPVGT 185  
Qy 430 RDMIEGTYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSDKRTLACLIQ 489  
Db 186 RDMIEGTYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSDKRTLACLIQ 245  
Qy 490 NFWPEDISVQWLHNEVOLPDARHSTTQPRKTKSGGFVFSRLVTRAWEQKDEFICRAV 549  
Db 246 NFWPEDISVQWLHNEVOLPDARHSTTQPRKTKSGGFVFSRLVTRAWEQKDEFICRAV 305  
Qy 550 HEAASPSQTVQRAVSNVPGK 569  
Db 306 HEAASPSQTVQRAVSNVPGK 325  
RESULT 2  
US-11-022-289-6  
; Sequence 6, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-6  
Query Match 49.6%; Score 1518; DB 7; Length 557;  
Best Local Similarity 53.2%; Pred. No. 6.9e-68;  
Matches 306; Conservative 47; Mismatches 100; Indels 122; Gaps 7;  
Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120  
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 218  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 278  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGKVEGGGSG 240  
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSPGK 330  
Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVD 300  
Db 331 -----DKHTC----- 330  
Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRITYTCQVTYQGHTEPDTSTKKCADSNPRGVS 360  
Db 331 ----- 330  
Qy 361 YLSRPSFPD-LFIKRSPTITCLVVDLAPSGVTNLTWSRAGKPVNHSIRKEKQKNGTL 419  
Db 351 FLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTY 410  
Qy 420 TVTSTLPVGTTRDMEGTQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSR 479  
Db 411 RVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSR 465

Qy 480 DKRT-----LACIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKSGGFVFSRLEV 534  
Db 466 DELTKNQVSLTCLVKGFYPSDIAVWESN--GQPENNYKTTTPVLDSDGSGFFLYSKLTVD 523  
Qy 535 RAWEQKQDEFICRAVHEAASPSQTVQRAVSNVPGK 569  
Db 524 KSRWQQGNVFCSCVMHEALHNYT-QKSLSPGK 557  
RESULT 3  
US-11-022-289-8  
; Sequence 8, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: Fc POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR APPLICATION NUMBER: US 60/531,752  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 551  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-8  
Query Match 49.4%; Score 1513; DB 7; Length 551;  
Best Local Similarity 53.2%; Pred. No. 1.2e-67;  
Matches 306; Conservative 47; Mismatches 94; Indels 128; Gaps 8;  
Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120  
Db 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 218  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 180  
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 278  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGKVEGGGSG 240  
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQKSLSPGK 330  
Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLCLVSGYTPGTINITWLEDQVMDVD 300  
Db 331 -----PPS-----PAPELL----- 339  
Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRITYTCQVTYQGHTEPDTSTKKCADSNPRGVS 360  
Db 340 ----- 344  
Qy 361 YLSRPSFPD-LFIKRSPTITCLVVDLAPSGVTNLTWSRAGKPVNHSIRKEKQKNGTL 419  
Db 345 FLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTY 404  
Qy 420 TVTSTLPVGTTRDMEGTQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSR 479  
Db 405 RVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSR 459  
Qy 480 DKRT-----LACIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKSGGFVFSRLEV 534  
Db 460 DELTKNQVSLTCLVKGFYPSDIAVWESN--GQPENNYKTTTPVLDSDGSGFFLYSKLTVD 517  
Qy 535 RAWEQKQDEFICRAVHEAASPSQTVQRAVSNVPGK 569



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; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-5

Query Match          49.4%; Score 1511; DB 7; Length 557;
Best Local Similarity 53.1%; Pred. No. 1.5e-67;
Matches 306; Conservative 48; Mismatches 98; Indels 124; Gaps 8;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKEPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NWYVDGVEVHNVTKEPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 240
DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 330
QY 241 GGGSGGGGFTPTVKILQSSCDGGGHPPTTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
DB 331 ----- 330
QY 301 LSTASTTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHTFEDSTKCK-ADSNPRGVS 359
DB 331 -----DKTHTC-----PPCPAPELLGGPS 349
QY 360 AYLRSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSTRKEEKORNGT 418
DB 350 VFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVTKEPREQYNST 409
QY 419 LTVTSPLPVGTRDWIGETVQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS 478
DB 410 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL-----PPS 464
QY 479 RDKRT-----LACLIONFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLRV 533
DB 465 RDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPVVLDSGSGFFLYSKLTV 522
QY 534 TRAEWEQKDEFICRAVHEAASPSQTVQRAVSNPGK 569
DB 523 DKSRWQQGNVFCFSVMHEALHNHYT-QKSLSLSPGK 557

RESULT 7
US-11-022-289-2
; Sequence 2, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185931/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-022-289-5

Query Match          49.4%; Score 1511; DB 7; Length 557;
Best Local Similarity 53.1%; Pred. No. 1.5e-67;
Matches 306; Conservative 48; Mismatches 98; Indels 124; Gaps 8;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKEPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NWYVDGVEVHNVTKEPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 240
DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 330
QY 241 GGGSGGGGFTPTVKILQSSCDGGGHPPTTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
DB 331 ----- 330
QY 301 LSTASTTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHTFEDSTKCK-ADSNPRGVS 359
DB 331 -----DKTHTC-----SPCPAPELLGGPS 349
QY 360 AYLRSRSPD-LFIRKSPITITCLVVDLAPSKGTNLTWSRASKGKPVNHSTRKEEKORNGT 418
DB 350 VFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVTKEPREQYNST 409
QY 419 LTVTSPLPVGTRDWIGETVQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGS 478
DB 410 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL-----PPS 464
QY 479 RDKRT-----LACLIONFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLRV 533
DB 465 RDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTTTPVVLDSGSGFFLYSKLTV 522
QY 534 TRAEWEQKDEFICRAVHEAASPSQTVQRAVSNPGK 569
DB 523 DKSRWQQGNVFCFSVMHEALHNHYT-QKSLSLSPGK 557

RESULT 8
US-11-022-289-3
; Sequence 3, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185931/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
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US-11-022-289-3

Query Match 48.9%; Score 1497.5; DB 7; Length 548;  
Best Local Similarity 52.3%; Pred. No. 6.7e-67;  
Matches 301; Conservative 49; Mismatches 94; Indels 131; Gaps 7;

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Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

Qy 61 NWTVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120
Db 159 NWTVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 218

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTP 180
Db 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTP 278

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 240
Db 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

Qy 241 GGGSGGGSTPTPTVKILOSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVD 300
Db 331 GGGSGGGSTPTPTVKILOSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVD 336

Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKCKADSNPRGVA 360
Db 337 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKCKADSNPRGVA 341

Qy 361 YLSRPSFDLFIKRSPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKORNGTL 419
Db 342 FLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWVDGVEVHNVTKPREEQYNSTY 401

Qy 420 TVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSR 479
Db 402 RVSVSLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL-----PPSR 456

Qy 480 DKRT-----LACLONFMPEDISVQWLHNEVQLPDARHSTTQPKTKGSGFFVFSRLEVT 534
Db 457 EEMTKNQVSLTCLVKGYFSPDSIAVEWESN--GQPENNYKTTTPPVLDSVGSFFLYSKLTV 514

Qy 535 RAWEQKDEFICRAVHEAASPSQTVQRAVSNPGK 569
Db 515 KSRWQGNVFSCVMHEALHNHYT-QKSLSLSPGK 548
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RESULT 9

US-11-022-289-10  
; Sequence 10, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR FILING DATE: 2004-12-21  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 10  
; LENGTH: 564  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-11-022-289-10

Query Match 46.2%; Score 1412.5; DB 7; Length 564;  
Best Local Similarity 52.0%; Pred. No. 8.7e-63;  
Matches 298; Conservative 37; Mismatches 127; Indels 111; Gaps 10;

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Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

Qy 61 NWTVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120
Db 159 NWTVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 218

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTP 180
Db 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTP 278

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 240
Db 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 334

Qy 241 GGGSGGGSTPTPTVKILOSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVD 300
Db 335 GGGSGGGSTPTPTVKILOSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVD 351

Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKCKADSNPRGVA 360
Db 352 LSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQGHTFEDSTKCKADSNPRGVA 356

Qy 361 YLSRPSFDLFIKRSPTITCLVVDLAPSKGTNLTWSRAGKPVNHSRKEEKORNGTL 420
Db 357 SLHRPALEDLLGSEANLTCTLTGLRDASG-VITFTWTFPSGKSAVQG--PPERDLGCGYS 413

Qy 421 VTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTSGPRAAPEVYAFATP-EWPGSR 479
Db 414 VSSVLPGCABPMNHGKTFTCTAAYPE-SKTPTLTATLSKSGNTTPRPEVHLLPPSEELALN 472

Qy 480 DKETLACLIONFMPEDISVQWLHNEVQLPDARHSTTQPKTKGSG---FFVFSRLEVTRA 536
Db 473 ELVTLTCLAGFPKQVLRWLGQSQELPREKLTWASRQSPSQGTTTFAVTSILRVAAE 532

Qy 537 EWBQKDEFICRAVHEAASPSQTVQRAVSNPGK 569
Db 533 DWKKGDTFSCWVGHEAL-PLAFTQKTIDRLAGK 564
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RESULT 10

US-11-022-289-11  
; Sequence 11, Application US/11022289  
; Publication No. US20050249723A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazar, Gregory Alan  
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL Fc LIGAND BINDING SITES  
; FILE REFERENCE: 185831/US/2  
; CURRENT APPLICATION NUMBER: US/11/022,289  
; CURRENT FILING DATE: 2004-12-21  
; PRIOR FILING DATE: 2004-12-21  
; PRIOR FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-022-289-11

Query Match 40.0%; Score 1225; DB 7; Length 330;  
Best Local Similarity 97.0%; Pred. No. 6.5e-54;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

Qy 61 NWTVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQWMNMGKEYCKVSNKALPAPIEKT 120
Db 159 NWTVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 218
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Qy	121	ISKAKVQPREPQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPP	180
Db	219	ISKAKVQPREPQVYTLPPSRDELTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPP	278
Qy	181	PVLDSVGSFPLYSKLTVDKSRWQGNVFCSCWMEALHNNHYQQRSLSLSPGK	232
Db	279	PVLDSGSPFLYSKLTVDKSRWQGNVFCSCWMEALHNNHYTKSLSLSPGK	330

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RESULT 11
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

```

RESULT 12  
US-11-016-503-6  
; Sequence 6, Application US/11016503  
; Publication No. US20050245447A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING THEREOF  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016,503  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/009,852

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; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-503-6

Query Match      40.0%; Score 1235; DB 7; Length 452;
Best Local Similarity 97.0%; Pred. No. 8.4e-54;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1  EPKSCDKTHCTCPCPAPELIGGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKF 60
        |||
Db      221 EPKSCDKTHCTCPCPAPELIGGSVFLFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKF 280

Qy      61  NWTVDGVGEVHNVTKPREEQYNSTYRVSVLTVLHQNWNGKEYCKKVSNKALPAPIEKT 120
        |||
Db      281 NWTVDGVGEVHNANTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKKVSNKALPAPIEKT 340

Qy      121 ISKAKVQPREPOVYTLPPSDELTKNQVSLTCLVKGFPSPDIAVEESNGQPENNYKTT 180
        |||
Db      341 ISKAKGQPREPOVYTLPPSDELTKNQVSLTCLVKGFPSPDIAVEESNGQPENNYKTT 400

Qy      181 PVLDSVGSFPFLYSKLTVDKSRWQGNVFCSVMHREALHNHYQOQSLSLSPGK 232
        |||
Db      401 PVLDSGSPFLYSKLTVDKSRWQGNVFCSVMHREALHNHYTKQSLSLSPGK 452

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RESULT 13
US-10-949-720-390
; Sequence 390, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949, 720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390

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[illegible]

Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHONMMNGKEYCKVSNKALPAPIEKT 120  
Db 288 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHONMMNGKEYCKVSNKALPAPIEKT 347  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
Db 348 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 407  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSLSPGK 232  
Db 408 PVLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSLSPGK 459

RESULT 14

US-11-016-503-8  
; Sequence 8, Application US/11016503  
; Publication No. US20050245447A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING THEREOF  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016.503  
; PRIOR FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 462  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-016-503-8

Query Match 40.0%; Score 1225; DB 7; Length 462;  
Best Local Similarity 97.0%; Pred. No. 8.6e-54;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 231 EPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 290  
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHONMMNGKEYCKVSNKALPAPIEKT 120  
Db 291 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHONMMNGKEYCKVSNKALPAPIEKT 350  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
Db 351 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 410  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSLSPGK 232  
Db 411 PVLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSLSPGK 462

RESULT 15

US-10-835-475-11  
; Sequence 11, Application US/10835475  
; Publication No. US20050244410A1  
; GENERAL INFORMATION:  
; APPLICANT: Centocor, Inc.  
; TITLE OF INVENTION: Toll-Like Receptor Binding Agents and Uses Thereof  
; FILE REFERENCE: CEN5022 USNP  
; CURRENT APPLICATION NUMBER: US/10/835,475  
; CURRENT FILING DATE: 2004-04-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11

; LENGTH: 489  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Predicted Mature Form of TLR9 EC260-Fc Fusion  
US-10-835-475-11  
Query Match 40.0%; Score 1225; DB 1; Length 489;  
Best Local Similarity 96.1%; Pred. No. 9e-54;  
Matches 224; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 PKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 61  
Db 238 PKSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 297  
Qy 62 WYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHONMMNGKEYCKVSNKALPAPIEKT 121  
Db 298 WYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHONMMNGKEYCKVSNKALPAPIEKT 357  
Qy 122 SKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 181  
Db 358 SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 417  
Qy 182 VLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSLSPGKVE 234  
Db 418 VLDSVGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYQORSLSLSPGKID 470  
Search completed: November 30, 2005, 00:46:53  
Job time : 13 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 30, 2005, 00:32:33 ; Search time 168 Seconds  
(without alignments)  
1415.148 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHTCPCPAPPELL.....HEAASPSQTVQRAVSNVNGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3060	100.0	569	3	US-09-847-208-7
2	3060	100.0	569	4	US-10-000-439-7
3	1775	58.0	574	4	US-10-047-542-45
4	1775	58.0	574	4	US-10-214-524-37
5	1775	58.0	574	4	US-10-050-902-176
6	1775	58.0	574	4	US-10-050-898-176
7	1766	57.7	427	3	US-09-847-208-5
8	1766	57.7	427	4	US-10-000-439-5
9	1766	57.7	428	3	US-09-916-230-1
10	1766	57.7	428	3	US-09-949-375A-1
11	1766	57.7	428	4	US-10-047-542-60
12	1766	57.7	428	4	US-10-363-954A-1
13	1755	57.4	441	3	US-09-949-375A-7
14	1755	57.4	441	4	US-10-363-954A-7
15	1754.5	57.3	497	5	US-10-872-932A-35
16	1754.5	57.3	497	5	US-10-810-881A-34
17	1754.5	57.3	497	5	US-10-981-936-34
18	1733.5	56.7	586	5	US-10-627-556-384
19	1729	56.5	592	4	US-10-207-655-334
20	1729	56.5	592	5	US-10-627-556-129
21	1727	56.4	648	5	US-10-627-556-180
22	1725.5	56.4	648	5	US-10-627-556-184
23	1725	56.4	635	5	US-10-627-556-176
24	1721.5	56.3	593	5	US-10-627-556-248
25	1707	55.8	320	3	US-09-847-208-6
26	1707	55.8	320	4	US-10-000-439-6
27	1707	55.8	323	3	US-09-949-375A-2

## ALIGNMENTS

### RESULT 1

US-09-847-208-7

; Sequence 7, Application US/09847208

; Publication No. US20030082190A1

; GENERAL INFORMATION:

; APPLICANT: Saxon, Andrew

; APPLICANT: Zhang, Ke

; APPLICANT: Zhu, Daocheng

; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF

; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES

; FILE REFERENCE: UC67.002A

; CURRENT APPLICATION NUMBER: US/09/847,208

; CURRENT FILING DATE: 2001-05-01

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: fastseq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 569

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IGG1) to CH2-CH3-CH4

; OTHER INFORMATION: (IGF)

; US-09-847-208-7

Query Match 100.0%; Score 3060; DB 3; Length 569;  
Best Local Similarity 100.0%; Pred. No. 5.5e-193;  
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EPKSCDKTHTCPCPAPPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKF	60
DB	1	EPKSCDKTHTCPCPAPPELLGGPSVFLPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKF	60
QY	61	NWYVDGVEVHNKPKPEEQNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT	120
DB	61	NWYVDGVEVHNKPKPEEQNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT	120
QY	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKPTP	180
DB	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKPTP	180
QY	181	PVLDVSGGFFLYSKLTVDKSRWQQGNVSCSMVHEALHNHYQOQSLSLSPGKVEGGGSG	240
DB	181	PVLDVSGGFFLYSKLTVDKSRWQQGNVSCSMVHEALHNHYQOQSLSLSPGKVEGGGSG	240
QY	241	GGSGGGGSPPTVKILQSCDGGHFPPTIQLCLVSGYTPGTINTLTWLDGQVMDVD	300
DB	241	GGSGGGGSPPTVKILQSCDGGHFPPTIQLCLVSGYTPGTINTLTWLDGQVMDVD	300
QY	301	LSTASTTQEGELASTQSELTLSQKHWSLDRITYTCQVYQGHFTFEDSTKCADSNPRGVA	360
DB	301	LSTASTTQEGELASTQSELTLSQKHWSLDRITYTCQVYQGHFTFEDSTKCADSNPRGVA	360

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Db 301 LSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQGHTEPDSSTKKCADSNPRGVS 360
Qy 361 YLSRPSFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLT 420
Db 361 YLSRPSFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLT 420
Qy 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480
Db 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480
Qy 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540
Db 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540
Qy 541 KDEFICRAVHEAASPSTQVORAVSVNPGK 569
Db 541 KDEFICRAVHEAASPSTQVORAVSVNPGK 569

RESULT 2
US-10-000-439-7
; Sequence 7, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (Ige) sequence
US-10-000-439-7

Query Match 100.0%; Score 3060; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.5e-193;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNVTKPREQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNVTKPREQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120

Qy 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTP 180
Db 121 ISRAKVPREPQVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNHY-QRSLSLSLSPGKVEGGSG 240
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNHY-QRSLSLSLSPGKVEGGSG 240

Qy 241 GGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300
Db 241 GGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQVMDVD 300

Qy 301 LSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQGHTEPDSSTKKCADSNPRGVS 360
Db 301 LSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQGHTEPDSSTKKCADSNPRGVS 360
Qy 361 YLSRPSFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLT 420
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Db 361 YLSRPSFDLFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQKNGTLT 420
Qy 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480
Db 421 VTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRD 480
Qy 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540
Db 481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTRAWEQ 540
Qy 541 KDEFICRAVHEAASPSTQVORAVSVNPGK 569
Db 541 KDEFICRAVHEAASPSTQVORAVSVNPGK 569

RESULT 3
US-10-047-542-45
; Sequence 45, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-45

Query Match 58.0%; Score 1775; DB 4; Length 574;
Best Local Similarity 77.3%; Pred. No. 2e-108;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Qy 120 TTSKAKVQREPQVYTLPPSRDELTKNOVSLT--CLVKGYFSPSDIAVEWESNGQPENNYK 177
Db 143 TVSSASTQ--SPSVFPLTRCKNIPSNATSVLGLCLATGTFPEPVMTWDT--GSLNGTTM 199

Qy 178 TTP-PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSVNHEALHNHY-QRSLSLSLSPGKVEG 235
Db 200 TLPATTTLSGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSDWDVNKTFVC----- 251

Qy 236 GGGSGGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINTWLEDGQ 295
Db 252 -----SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINTWLEDGQ 300

Qy 296 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQGHTEPDSSTKKCADSNP 355
Db 301 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRYTCQVYQGHTEPDSSTKKCADSNP 360

Qy 356 RGVSAVLSRPSPPDLFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQ 415
Db 361 RGVSAVLSRPSPPDLFIKSPPTITCLVVDLAPSKGTVNLTWRSASGKPVNHSRKEEKQ 420

Qy 416 NGTLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEW 475
Db 421 NGTLTVTSTLPVGTDRDWEGETYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEW 480

Qy 476 PGSRDKRTKLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTR 535
Db 481 PGSRDKRTKLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGGFFVFSRLEVTR 540
Qy 536 AEWEQKDEFICRAVHEAASPSTQVORAVSVNPGK 569
```

```
Db 541 AEWEQKDEFCRAVHEAASPSQTVORAVSNPGK 574
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 176
; LENGTH: 574
; TYPE: PRT
; ORGANISM: IGE heavy chain
US-10-050-902-176

Query Match 58.0%; Score 1775; DB 4; Length 574;
Best Local Similarity 77.3%; Pred. No. 2e-108;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

RESULT 4
US-10-214-524-37
; Sequence 37, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Human (Homo sapiens)
US-10-214-524-37

Query Match 58.0%; Score 1775; DB 4; Length 574;
Best Local Similarity 77.3%; Pred. No. 2e-108;
Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

Db 120 TISKAKVQPREQVYTLPPSRDELTKNOVSLT--CLVKGFPSPDIAVEWESNGQPENNYK 177
Db 143 TVSSASTQ--SPSVFPLTRCKKNIPSNATSVTLGCLATGYFPEPVMTWDT--GSLNGTMM 199
Qy 178 TTP-PVLDSVSGFFLYSKLTVDKSRWQGNVFSVSMHEALHNNH-Y-QORSLSLSPGKVEG 235
Db 200 TLPATTLTSLGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 251
Qy 236 GGGSGGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQ 295
Db 252 -----SRDTPPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQ 300
Qy 296 VMDVDLSTASTTOGELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNP 355
Db 301 VMDVDLSTASTTOGELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNP 360
Qy 356 RGVSAYLRSRPFDFIRKSPITITCLVVDLAPSKGTVNLTWRSRASKGKPVNHSRKEEKOR 415
Db 361 RGVSAYLRSRPFDFIRKSPITITCLVVDLAPSKGTVNLTWRSRASKGKPVNHSRKEEKOR 420
Qy 416 NGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 475
Db 421 NGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 480
Qy 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535
Db 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540
Qy 536 AEWEQKDEFCRAVHEAASPSQTVORAVSNPGK 569
Db 541 AEWEQKDEFCRAVHEAASPSQTVORAVSNPGK 574

RESULT 5
US-10-050-902-176
; Sequence 176, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer

Db 120 TISKAKVQPREQVYTLPPSRDELTKNOVSLT--CLVKGFPSPDIAVEWESNGQPENNYK 177
Db 143 TVSSASTQ--SPSVFPLTRCKKNIPSNATSVTLGCLATGYFPEPVMTWDT--GSLNGTMM 199
Qy 178 TTP-PVLDSVSGFFLYSKLTVDKSRWQGNVFSVSMHEALHNNH-Y-QORSLSLSPGKVEG 235
Db 200 TLPATTLTSLGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 251
Qy 236 GGGSGGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQ 295
Db 252 -----SRDTPPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDGQ 300
Qy 296 VMDVDLSTASTTOGELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNP 355
Db 301 VMDVDLSTASTTOGELASTQSELTLSQKHWLSDRITYTCQVYQGHTEFEDSTKKCADSNP 360
Qy 356 RGVSAYLRSRPFDFIRKSPITITCLVVDLAPSKGTVNLTWRSRASKGKPVNHSRKEEKOR 415
Db 361 RGVSAYLRSRPFDFIRKSPITITCLVVDLAPSKGTVNLTWRSRASKGKPVNHSRKEEKOR 420
Qy 416 NGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 475
Db 421 NGTLTVTSTLPVGTDRDIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW 480
Qy 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535
Db 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540
Qy 536 AEWEQKDEFCRAVHEAASPSQTVORAVSNPGK 569
Db 541 AEWEQKDEFCRAVHEAASPSQTVORAVSNPGK 574

RESULT 6
US-10-050-898-176
; Sequence 176, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer
```





186 VGSFPLSKLTVDKSRWQGNVFCVSMHEALHNHY - QORSLSLSPGKVEGGGGGGGS 244  
62 SGHATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 104  
245 GGGGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 304  
105 --SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 162  
305 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 364  
163 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 222  
365 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQNGTLTVTST 424  
223 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQNGTLTVTST 282  
425 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484  
283 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 342  
485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 544  
343 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 402  
545 ICRAVHEAASPSQTVQRAVSNVPGK 569  
403 ICRAVHEAASPSQTVQRAVSNVPGK 427

## RESULT 9

US-09-916-230-1  
; Sequence 1, Application US/09916230  
; Patent No. US20020146422A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F.  
; TITLE OF INVENTION: Compositions for Inducing Self-Specific Anti-IgE  
; FILE REFERENCE: 1700.0140801  
; CURRENT APPLICATION NUMBER: US/09/916,230  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: US 60/221,841  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-916-230-1

Query Match 57.7%; Score 1766; DB 3; Length 428;  
Best Local Similarity 78.0%; Pred. No. 5.6e-108;  
Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;  
129 REPQVTLPPSRDELTKNOVSLT-CLVKGFPVPSDIAVEWESNGQEPNNYKTP-PVLDS 185  
4 QSPSVFPLRCCKNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTMTLPATLTL 62  
186 VGSFPLSKLTVDKSRWQGNVFCVSMHEALHNHY - QORSLSLSPGKVEGGGGGGGS 244  
63 SGHATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 105  
245 GGGGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 304  
106 --SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 163  
305 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 364  
164 STTQEGELASTQSELTLQKHWLSDRTYTCQVYQGHFTFEDSTKCADSNPRGVSAYLSR 223  
365 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQNGTLTVTST 424

Db 224 PSPFLDFIRKSPITICLVVDLAPSGTGNLTWSRASGKPVNHSRKKEKQNGTLTVTST 283  
Qy 425 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484  
Db 284 LPVGTDRWIEGTQYQCRVTHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343  
Qy 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 544  
Db 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLLEVTRAWEQKDEF 403  
Qy 545 ICRAVHEAASPSQTVQRAVSNVPGK 569  
Db 404 ICRAVHEAASPSQTVQRAVSNVPGK 428

## RESULT 10

US-09-949-375A-1  
; Sequence 1, Application US/09949375A  
; Patent No. US20020172673A1  
; GENERAL INFORMATION:  
; APPLICANT: KLYSNER, Steen et al.  
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE  
; FILE REFERENCE: 3631-0111P  
; CURRENT APPLICATION NUMBER: US/09/949,375A  
; CURRENT FILING DATE: 2002-01-18  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (11)..(116)  
; OTHER INFORMATION: Human IgE heavy chain C1 domain  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (209)..(216)  
; OTHER INFORMATION: Linker between domains C2 and C3  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (205)..(219)  
; OTHER INFORMATION: Epitope including C2C3 linker  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (315)..(323)  
; OTHER INFORMATION: Epitope including C3C4 linker  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (244)..(251)  
; OTHER INFORMATION: Epitope in BC loop  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (272)..(280)  
; OTHER INFORMATION: Epitope in DE loop  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (301)..(311)  
; OTHER INFORMATION: Epitope in FG loop  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (317)..(320)  
; OTHER INFORMATION: Linker between domains C3 and C4  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (321)..(422)  
; OTHER INFORMATION: Human IgE heavy chain C4 domain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (217)..(316)  
; OTHER INFORMATION: Human IgE heavy chain C3 domain  
; FEATURE:  
; NAME/KEY: DOMAIN





Db 224 PPSFDLFIKSPITICLVVDLAPSGKGVNUTWSRAGKPVNHSRKEEKORNGTLTVTST 283  
Qy 425 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484  
Db 284 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343  
Qy 485 ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 544  
Db 344 ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 403  
Qy 545 ICRVHAEAAASPSQTVQRAVSNP 567  
Db 404 ICRVHAEAAASPSQTVQRAVSNP 426

RESULT 14  
US-10-363-954A-7  
; Sequence 7, Application US/10363954A  
; Publication No. US20040156838A1  
; GENERAL INFORMATION:  
; APPLICANT: KLYSNER, Steen et al.  
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE  
; FILE REFERENCE: 4614-0115P  
; CURRENT APPLICATION NUMBER: US/10/363,954A  
; CURRENT FILING DATE: 2003-03-06  
; PRIOR APPLICATION NUMBER: US 60/232,831  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: DK PA 2000 01326  
; PRIOR FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (11)..(106)  
; OTHER INFORMATION: Ige heavy chain C1 domain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (113)..(208)  
; OTHER INFORMATION: Ige heavy chain C2 domain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (217)..(317)  
; OTHER INFORMATION: Ige heavy chain C3 domain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (321)..(422)  
; OTHER INFORMATION: Ige heavy chain C4 domain  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (427)..(441)  
; OTHER INFORMATION: MIGIS fragment  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (209)..(216)  
; OTHER INFORMATION: Linker between domains C2 and C3  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (318)..(320)  
; OTHER INFORMATION: Linker between domains C3 and C4  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (205)..(219)  
; OTHER INFORMATION: Epitope including C2C3 linker  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (315)..(323)  
; OTHER INFORMATION: Epitope including C3C4 linker  
; FEATURE:

; NAME/KEY: MISC FEATURE  
; LOCATION: (244)..(251)  
; OTHER INFORMATION: Epitope in BC loop  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (272)..(280)  
; OTHER INFORMATION: Epitope in DE loop  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (301)..(311)  
; OTHER INFORMATION: Epitope in FG loop  
US-10-363-954A-7  
Query Match 57.4%; Score 1755; DB 4; Length 441;  
Best Local Similarity 77.9%; Pred. No. 3.1e-107;  
Matches 345; Conservative 17; Mismatches 57; Indels 24; Gaps 7;  
Qy 129 REPOVYTLPPSRDELTKNOVSLT--CLVKGFPVPSDIAVWESNGQPENNYKTP-PVLDS 185  
Db 4 QSPSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMTWDT- GSLNGTTMTLPATTLTL 62  
Qy 186 VGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYH-QQRSLSLSLSPKVEGGGGGGGS 244  
Db 63 SGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVNDKTFVC----- 105  
Qy 245 GGGGFTPTVKILQSSCDGGGHPPTIQLCLVSGYTGTTINITWLEQVMDVDLSTA 304  
Db 106 --SRDFTPTVKILQSSCDGGGHPPTIQLCLVSGYTGTTINITWLEQVMDVDLSTA 163  
Qy 305 STTQEGELASTOSELTLSOKHLSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAVLSR 364  
Db 164 STTQEGELASTOSELTLSOKHLSLDRYTCQVYQGHTEFEDSTKCCADSNPRGVSAVLSR 223  
Qy 365 PSPFDLFIKSPITICLVVDLAPSGKGVNUTWSRAGKPVNHSRKEEKORNGTLTVTST 424  
Db 224 PSPFDLFIKSPITICLVVDLAPSGKGVNUTWSRAGKPVNHSRKEEKORNGTLTVTST 283  
Qy 425 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484  
Db 284 LPVGTDRDWEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343  
Qy 485 ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 544  
Db 344 ACLIQNFMPEDISVQWLHNEVOLPDARHSTTQPRKTKGSGFFVFSRLLEVTRAWEQKDEF 403  
Qy 545 ICRVHAEAAASPSQTVQRAVSNP 567  
Db 404 ICRVHAEAAASPSQTVQRAVSNP 426  
RESULT 15  
US-10-872-932A-35  
; Sequence 35, Application US/10872932A  
; Publication No. US20050033029A1  
; GENERAL INFORMATION:  
; APPLICANT: Jin lu  
; TITLE OF INVENTION: ENGINEERED ANTI-TARGET IMMUNOGLOBULIN DERIVED PROTEINS  
; FILE REFERENCE: CEN5031NP  
; CURRENT APPLICATION NUMBER: US/10/872,932A  
; CURRENT FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/483,654  
; PRIOR FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 35  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-872-932A-35  
Query Match 57.3%; Score 1754.5; DB 5; Length 497;  
Best Local Similarity 77.5%; Pred. No. 3.8e-107;  
Matches 347; Conservative 17; Mismatches 57; Indels 27; Gaps 8;



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 29, 2005, 23:38:37 ; Search time 189 Seconds

(without alignments)  
1322.786 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHCPCPAPELL.....HEAAPSQTQVRAVSNPGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3060	100.0	569	AAO19668	Aao19668 GE2 fusio
2	1775	58.0	574	ABG94250	Abg94250 Human Ige
3	1775	58.0	574	ABG80562	Abg80562 Human Ige
4	1775	58.0	574	ABP96592	Abp96592 Human Ige
5	1775	58.0	574	ADP97368	Adp97368 Human imm
6	1766	57.7	427	AAO19666	Aao19666 Human Ige
7	1766	57.7	428	AAW47863	Aaw47863 Human Ige
8	1766	57.7	428	AAU80283	Aau80283 Human Ige
9	1766	57.7	428	AAW50940	Aaw50940 Human Ige
10	1766	57.7	428	AAE35113	Aae35113 Human imm
11	1766	57.7	428	ADP48440	Adp48440 Human Pro
12	1766	57.7	428	ADP97382	Adp97382 Human Ige
13	1760	57.5	493	AAW40065	Aaw40065 Sequence
14	1755	57.4	441	AAU80287	Aau80287 Human Ige
15	1754.5	57.3	497	ADW24784	Adw24784 Human var
16	1754.5	57.3	497	ADW24742	Adw24742 Human var
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18	1754.5	57.3	497	ADZ08940	Adz08940 Mammalian
19	1754.5	57.3	497	ADZ44466	Adz44466 Human imm
20	1754.5	57.3	497	AEA16541	Aea16541 Human MCP
21	1754.5	57.3	497	AEB72776	Aeb72776 Anti-Ltal
22	1733.5	56.7	586	ADY22009	Ady22009 Antibody
23	1729	56.5	592	ADZ25773	Adz25773 Binding d
24	1729	56.5	592	ADY21754	Ady21754 Antibody

25	1727	56.4	648	9	ADY21805	Ady21805 Antibody
26	1725.5	56.4	648	9	ADY21809	Ady21809 Antibody
27	1725	56.4	635	9	ADY21801	Ady21801 Antibody
28	1723	56.3	428	2	AAR42950	Aar42950 Human IGE
29	1721.5	56.3	593	9	ADY21873	Ady21873 Antibody
30	1720.5	56.2	425	6	AAE35114	Aae35114 Human imm
31	1707	55.8	320	6	AAO19667	Aao19667 Human IGE
32	1707	55.8	323	5	AAU80286	Aau80286 Human IGE
33	1707	55.8	323	5	AAU80285	Aau80285 Human IGE
34	1707	55.8	323	5	AAU80284	Aau80284 Human IGE
35	1707	55.8	324	2	AAR83559	Aar83559 Fc(eps)ilo
36	1707	55.8	325	2	AAR75225	Aar75225 Human IGE
37	1707	55.8	325	2	AAR77241	Aar77241 Human IGE
38	1707	55.8	327	9	ADY21849	Ady21849 Human IGE
39	1707	55.8	331	3	AAO303642	Aao303642 Human IGE
40	1707	55.8	331	7	ADD25768	Add25768 Binding d
41	1707	55.8	331	9	ADY21799	Ady21799 Human IGE
42	1707	55.8	331	9	ADY21722	Ady21722 Human IGE
43	1707	55.8	367	1	AAP80291	Aap80291 Interleuk
44	1705.5	55.7	426	6	ABP96581	Abp96581 Chimpanze
45	1701	55.6	325	3	AAW79994	Aaw79994 Human imm

ALIGNMENTS

RESULT 1

AAO19668  
ID AAO19668 standard; protein; 569 AA.

XX AC AAO19668;

XX DT 28-MAR-2003 (first entry)

XX DE GE2 fusion protein for use in treating immune diseases.

XX KW Human; IGE; immunoglobulin E; immunotherapy; immune disease;  
XX KW Fcepsilon receptor; autoimmune disease; constant region; heavy chain;  
XX KW antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2;  
XX KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;  
XX KW fusion protein.

XX OS Synthetic.

XX OS Unidentified.

XX PW WO200288317-A2.

XX PD 07-NOV-2002.

XX PF 01-MAY-2002; 2002WO-US013527.

XX PR 01-MAY-2001; 2001US-00847208.

XX PR 24-OCT-2001; 2001US-00000439.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

XX DR New fusion molecules comprising polypeptide sequences that bind to IgG  
XX PT inhibitory receptor and native IGE receptor, usefull for treating IGE-  
XX PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX PT autoimmune diseases.

XX PS Claim 35; Fig 7; 116pp; English.

XX CC The present invention relates to a fusion molecule comprising a first  
XX CC polypeptide sequence capable of specific binding to a native IGE  
XX CC inhibitory receptor consisting of an immune receptor tyrosine-based  
XX CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
XX CC functionally connected to a second polypeptide sequence capable of  
XX CC specific binding directly or indirectly to a native IGE receptor

CC	(FcepsilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IGE-mediated biological response, preferably an IGE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-1 diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is a gammahinge-CHgamma2-CHgamma3-(Gly4Ser)3-Chepsilon2-Chepsilon3-Chepsilon3 fusion protein (designated GB2) of the invention	OS	Homo sapiens.
CC		OS	Synthetic.
CC		PN	WO200256905-A2.
CC		XX	25-JUL-2002.
CC		XX	21-JAN-2002; 2002WO-IB000166.
CC		XX	19-JAN-2001; 2001US-0262379P.
CC		PR	04-MAY-2001; 2001US-0288549P.
CC		PR	05-OCT-2001; 2001US-0326998P.
CC		PR	07-NOV-2001; 2001US-0331045P.
CC		XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.
CC		PA	Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P; Piossek C;
CC		PI	WPI; 2002-627351/67.
CC		DR	Molecular antigen array used in the production of vaccines for infectious diseases.
CC		PT	Disclosure; Page 389-390; 441pp; English.
CC		XX	This invention relates to a novel ordered and repetitive antigen array used in the production of vaccines for infectious diseases. The invention also discloses a composition comprising a non-natural molecular scaffold comprising a core particle selected from a core particle of a non-natural origin and a core particle of natural origin and an organiser comprising at least one first attachment site, where the organiser is connected to the core particle by at least one covalent bond. Also disclosed is an antigen or antigenic determinant with at least one second attachment site, where the antigen or antigenic determinant is amyloid beta peptide (Abetal-42) or its fragment and where the second attachment site is selected from an attachment site not naturally occurring with the antigen or antigenic determinant and an attachment site naturally occurring with the antigen or antigenic determinant, where the second attachment site is capable of association through at least one non-peptide bond to the first attachment site and where the antigen or antigenic determinant and the scaffold interact through the association to form an ordered and repetitive antigen array. The invention also comprises a coat protein capable of forming a capsid which comprises mutant Qbeta coat proteins having an amino acid sequence selected from five amino acid sequences fully defined in the specification. The compounds of the invention may have antimicrobial, antiallergic, immunomodulatory, cytostatic, antiviral, antidiabetic, or hypoglycaemic activities and may be used in immunisation and as a vaccine. The present sequence represents a protein sequence used to create the compositions of the invention
CC		XX	Sequence 574 AA;
CC		XX	Query Match 58.0%; Score 1775; DB 5; Length 574;
CC		XX	Best Local Similarity 77.3%; Pred. No. 5.6e-114; Indels 26; Gaps 8;
CC		XX	Matches 351; Conservative 17; Mismatches 60;
CC		QY	120 TISKAKVQPREPQVYTLPPSRDELTKNQVSLT-CLVKGFPYSDIAVWESNGQPENNYK 177
CC		DB	143 TVSSASTQ--SPSVPLTRCKNIPSNATSVTLGCLATGYFPEPVNVTWDT-GSLNGTMM 199
CC		QY	178 TTP-PVLDSVGFYFLYKLTVDKSRWQGNVFCSCVMHEALHNHY-QQRSLSPKQVEG 235
CC		DB	200 TLPATTLTSLGSHYATISLLTV-SGAWAK-QMPTCRVAHTPSSTDMVDNKTFVSC----- 251
CC		QY	236 GGGSGGGSGGGSGTPTVKILQSCDGGGHPPTIQLCLVSGYTPGTINTLWEDGQ 295
CC		DB	252 -----SRDFTPTVKILQSCDGGGHPPTIQLCLVSGYTPGTINTLWEDGQ 300
CC		QY	296 VMDVLDLSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVTYQGHFTFEDSKKCADSNP 355
CC		DB	301 VMDVLDLSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVTYQGHFTFEDSKKCADSNP 360
CC		QY	1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
CC		DB	1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
CC		QY	61 NWVDGVEVHNVTKPREEQYNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120
CC		DB	61 NWVDGVEVHNVTKPREEQYNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKT 120
CC		QY	121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTP 180
CC		DB	121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTP 180
CC		QY	181 PVLDSVGSFPFLYKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGKVEGGGSG 240
CC		DB	181 PVLDSVGSFPFLYKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGKVEGGGSG 240
CC		QY	241 GGGSGGGSGTPTVKILQSCDGGGHPPTIQLCLVSGYTPGTINTLWEDGQVMDVD 300
CC		DB	241 GGGSGGGSGTPTVKILQSCDGGGHPPTIQLCLVSGYTPGTINTLWEDGQVMDVD 300
CC		QY	301 LSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVTYQGHFTFEDSKKCADSNPRGUSA 360
CC		DB	301 LSTASTTQEGELASTQSELTLSQKHWSLDRYTCQVTYQGHFTFEDSKKCADSNPRGUSA 360
CC		QY	361 YLSRSPDFDLIRKSPITITCLVLDLAPSKGTNLTWSRAGKPVNHSRKEEKQRNGTLT 420
CC		DB	361 YLSRSPDFDLIRKSPITITCLVLDLAPSKGTNLTWSRAGKPVNHSRKEEKQRNGTLT 420
CC		QY	421 VTSTLPVGTEDWIEGETYQCRVTHPHLPRALMRSTTKSGPRAAPVYAFATPEWPGSRD 480
CC		DB	421 VTSTLPVGTEDWIEGETYQCRVTHPHLPRALMRSTTKSGPRAAPVYAFATPEWPGSRD 480
CC		QY	481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVSRLEVTRAWEQ 540
CC		DB	481 KRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVSRLEVTRAWEQ 540
CC		QY	541 KDFICRAVHAASPSQTQVRAVSNPGK 569
CC		DB	541 KDFICRAVHAASPSQTQVRAVSNPGK 569
CC		XX	RESULT 2
CC		ID	ABG94250
CC		XX	ABG94250 standard; protein; 574 AA.
CC		AC	ABG94250;
CC		DT	10-DEC-2002 (first entry)
CC		XX	Human IgE heavy chain constant region peptide #1.
CC		XX	Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
CC		KW	cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
CC		KW	vaccine; infectious disease.
CC		XX	



QY 356 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKQ 415  
 DB 361 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKQ 420  
 QY 416 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 475  
 DB 421 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 480  
 QY 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535  
 DB 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540  
 QY 536 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 569  
 DB 541 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 574

## RESULT 3

ABG80562

ID ABG80562 standard; protein; 574 AA.

AC ABG80562;

DT 29-NOV-2002 (first entry)

DE Human IgE heavy chain.

KW Molecular antigen array; vaccine; antigen; antimicrobial;  
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;  
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.

XX Homo sapiens.

XX OS

XX PN WO200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.

XX 04-MAY-2001; 2001US-0288549P.

XX 05-OCT-2001; 2001US-0326998P.

XX 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX (NOVS) NOVARTIS PHARMA AG.

XX (MAUR/) MAURER P.

XX (LECH/) LECHNER F.

XX (ORTM/) ORTMANN R.

XX (LUEO/) LUEOEND R.

XX (STAU/) STAUFENBIEL M.

XX (FREY/) FREY P.

XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;

XX Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;

XX WPI; 2002-636514/68.

XX Molecular antigen array used in the production of vaccines for infectious

CC core particle of a non-natural origin; and (2) a core particle of natural  
 CC origin; and (ii) an organism comprising at least one first attachment  
 CC site, where the organism is connected to the core particle by at least  
 CC one covalent bond; (b) an antigen or antigenic determinant with at least  
 CC one second attachment site, where the antigen or antigenic determinant is  
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
 CC attachment site is selected from: (i) an attachment site not naturally  
 CC occurring with the antigen or antigenic determinant; and (ii) an  
 CC attachment site naturally occurring with the antigen or antigenic  
 CC determinant, where the second attachment site is capable of association  
 CC through at least one non-peptide bond to the first attachment site; and  
 CC where the antigen or antigenic determinant and the scaffold interact  
 CC through the association to form an ordered and repetitive antigen array.  
 CC Also included is a process for producing a non-naturally occurring  
 CC ordered and repetitive antigen array. The composition is used in  
 CC immunisation and as a vaccine for diseases such as influenza, graft  
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult  
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 CC gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 CC osteoporosis and infectious diseases. The present sequence is an antigen  
 CC for use in the array of the invention. The antigen is modified to possess  
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine- containing N-  
 CC or C-terminal linker peptide which serves as the attachment point to a  
 CC virus like particle or bacterial protein (the scaffold protein)

XX SQ Sequence 574 AA;

Query Match 58.0%; Score 1775; DB 5; Length 574;

Best Local Similarity 77.3%; Pred. No. 5.6e-114;

Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

QY 120 TISKAKVQPREPQVYTLPPSRDEITKQVSLT--CLVKGFPVSDIAVWENSGQENNVK 177

DB 143 TVSSASTQ--SPSVFPLTRCCNKIPSNATSVTLGLATGYPPEPVMVTDWDT-GSLNGTMM 199

QY 178 TTP-PVLDSVGSFFLYSKLTVDKSRWQGVNFCVSMHEALHNYH-QQRSLSLSPGKVEG 235

DB 200 TLPATTLTSLGHYATISLLTV-SGAWAK-QMPTCRVAHTPSTWDVNDKTSVC----- 251

QY 236 GGGGGGGGGGGGFTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDQ 295

DB 252 -----SRDFTPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDQ 300

QY 296 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQHTFEDSTKCADSNP 355

DB 301 VMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVYQHTFEDSTKCADSNP 360

QY 356 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKQ 415

DB 361 RGVSAVLSRSPFDLFIKSPPTITCLVVDLAPSGKTNLTWSRAGKPVNHSRKEEKQ 420

QY 416 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 475

DB 421 NGTLTVTSTLPGVTRDWEGETYQCRVTHPLPRALMRSTTKTGSPRAAPEVYAFATPEW 480

QY 476 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 535

DB 481 PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTR 540

QY 536 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 569

DB 541 ABEWQKDFICRAVHEAASPSQTVQRAVSVNPGK 574

## RESULT 4

ABP96592

ID ABP96592 standard; protein; 574 AA.

XX ABP96592;

AC ABP96592;

XX 28-MAY-2003 (first entry)

XX Human IgE heavy chain amino acid sequence SEQ ID NO:37.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;

XX immune response; major histocompatibility complex; MHC; immunogenic;

XX anti-allergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;

XX dermatological; antiinflammatory; IgE-mediated condition; food allergy;

XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;

XX urticaria hives.

XX Homo sapiens.

XX WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGET-) IGE THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response

XX against IgE, by identifying peptide eliciting CTL response to IgE

XX peptides naturally presented by major histocompatibility complex class I

XX protein.

XX Example 7; Page 174-177; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides

XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin

XX E (IgE), comprising providing a test peptide (T) suspected of being able

XX to bind to major histocompatibility complex (MHC) class I molecule, and

XX evaluating (T) for ability to elicit in a mammal a CTL response to

XX naturally processed and presented IgE peptides, where a peptide that

XX induces such a response is identified. Also described are compositions:

XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);

XX (C2) comprising at least one isolated polynucleotide encoding (I); and

XX (C3) comprising antigen-presenting cells that recognise at least one (I).

XX Where C1-3 are able to bind to at least one MHC class I molecule and to

XX elicit in a mammal a CTL response to naturally processed and presented

XX IgE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,

XX vasotropic, dermatological, antiinflammatory and cytostatic activities,

XX and can be used as inducers of a CTL response against IgE, and in

XX vaccines. C1-3 can be used for modulating an IgE-mediated condition in a

XX mammal. C1-3 are useful for modulating an IgE-mediated condition such as

XX IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic

XX hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are

XX useful for treating atopic hypersensitivity conditions (such as allergic

XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-

XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria

XX hives). The present sequence represents an IgE heavy chain amino acid

XX sequence, which is given in an example from the present invention

XX Sequence 574 AA;

SQ

Query Match 58.0%; Score 1775; DB 6; Length 574;

Best Local Similarity 77.3%; Pred. No. 5.6e-114;

Matches 351; Conservative 17; Mismatches 60; Indels 26; Gaps 8;

QY 120 TISKAKVQPEPOVYTLPPSRDELTKNQVSLT--CLVKGFPYSDIAVEWESNQPENNYK 177

Db 143 TVSSASTQ--SPGVFPLTRCKNIPSNATSVTLGCLATGYFPFVMTWDT-GSLNGTTM 199

QY 178 TTP-PVLDSVGSFPLYSLKLTVDKSRWQQGNVFCSVNMEALHNYH-QQRSLSLSPGKVEG 235

Db 200 TLPATTLTLSGHYATISLLTV-SGAWAK-QMFTCRVAHTPSSTDVDNKTFSVC----- 251

QY 236 GGGSGGGSGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQG 295

Db 252 -----SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQG 300

QY 296 VMDVDLSTASTTQEGELASTQSELTLUSQKHLSDRITYTCQVTVQGHTFEDSTKKCADSNP 355

Db 301 VMDVDLSTASTTQEGELASTQSELTLUSQKHLSDRITYTCQVTVQGHTFEDSTKKCADSNP 360

QY 356 RGVSAVLSRSPFDLFIKRSPTITCLVVDLAPS KGTVNLTWGRASGKPVNHSRKEEKQR 415

Db 361 RGVSAVLSRSPFDLFIKRSPTITCLVVDLAPS KGTVNLTWGRASGKPVNHSRKEEKQR 420

QY 416 NGTLTVTSTLPVGTROWIEGETYQCRVTHPHLPALMRSTTTKTSGRAPAEVYAFATPEW 475

Db 421 NGTLTVTSTLPVGTROWIEGETYQCRVTHPHLPALMRSTTTKTSGRAPAEVYAFATPEW 480

QY 476 PGSRDKRTIACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTR 535

Db 481 PGSRDKRTIACLIONFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLLEVTR 540

QY 536 AEWQKDEFICRAVHEAASPSQTQRAVSNPEK 569

Db 541 AEWQKDEFICRAVHEAASPSQTQRAVSNPEK 574

RESULT 5

ID ADE97368

XX ADE97368 standard; protein; 574 AA.

AC ADE97368;

XX

DT 12-FEB-2004 (first entry)

XX Human immunoadhesin-related protein - SEQ ID 45.

DE

XX immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;

KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;

KW intercellular adhesion molecule; ICAM-1; human.

XX

OS Homo sapiens.

XX WO2003064992-A2.

XX

PD 07-AUG-2003.

XX

PF 25-OCT-2002; 2002WO-US034197.

XX

PR 26-OCT-2001; 2001US-00047542.

XX (PLAN-) PLANET BIOTECHNOLOGY INC.

PA (LARR/) LARRICK J W.

PA (WYCO/) WYCOFF K L.

XX

PI Larrick JW, Wycoff KL;

XX WPI; 2003-636816/60.

DR

XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises

PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and

PT J chain and secretory component associated with the chimeric toxin

PT receptor protein.

XX Disclosure; SEQ ID NO 45; 288pp; English.

XX

XX The invention relates to a novel immunoadhesin comprising a chimeric

CC toxin receptor protein consisting of a toxin receptor protein linked to

CC at least a portion of an immunoglobulin heavy chain with a J (joining)

CC chain and secretory component (SC) associated with the chimeric toxin

CC receptor protein. The immunoadhesin comprises a chimeric bacterial or

CC viral toxin receptor protein and the immunoadhesin has plant-specific

CC glycosylation. The immunoadhesin of the invention demonstrates virucide





PI	Klyneser S, Von Hoegen P, Voldborg B, Gautam A;
XX	WPI; 2002-383033/41.
XX	
PT	Inducing immune response against autologous immunoglobulin E in an
PT	animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
PT	epitope an/or B-cell epitope derived from the immunoglobulin.
XX	
XX	Example; Page 101-103; 151pp; English.
XX	
CC	This invention relates to a novel method for inducing an immune response
CC	against autologous immunoglobulin E (IgE) in an animal. The method
CC	comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC	(CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
CC	epitope (TH epitope) which is foreign to the animal, by antigen
CC	presenting cells (APCs) of the animal's immune system. The epitopes of
CC	the invention may be used as a vaccine against allergic diseases. The
CC	method of the invention is useful for inducing an immune response against
CC	autologous IgE in an animal, which is useful for downregulating
CC	autologous IgE in the animal. This method is useful in the prevention and
CC	treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC	asthma and atopic dermatitis. The present sequence represents the human
CC	IgE heavy chain C1-C2-C3-C4 domains used to create the epitopes of the
CC	invention
XX	
SQ	Sequence 428 AA;
	Query Match 57.7%; Score 1766; DB 5; Length 428;
	Best Local Similarity 78.0%; Pred. No. 1.6e-113;
	Matches 347; Conservative 17; Mismatches 57; Indels 24; Gaps 7
QY	129 REPQYVTLPPSRDELTKNQVSLT-CLVKGFGYPSDIAVESWGQPPENNYKTP-PVLDS 185
DB	4 QSPSVEPLTRCCNIPSNATSVTLGCLATGYFPEPVMVTWDT-GSLNGTITLTPATLTLL 62
QY	186 VGSFPLYSKLTVDKSRWQGVFCVSWHEALHNYH-QQRSLSLSPKVEGGGSGGGGS 244
DB	63 SGHYATISLITV-SGAWAK-QMFTCRVAHTPSSTDWVDNKTFSVC----- 105
QY	245 GGGGSGFTPTTKVILQSSCDGGGHPPTTQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 304
DB	106 --SRDFTPTTKVILQSSCDGGGHPPTTQLLCLVSGYTPGTINITWLEDQVMDVDLSTA 163
QY	305 SITQBGELASTQSELTLQKHWLSDRYTVCQVYQGHTFEDSTKKCADSNPRGVSAYLRS 364
DB	164 SITQBGELASTQSELTLQKHWLSDRYTVCQVYQGHTFEDSTKKCADSNPRGVSAYLRS 223
QY	365 PSFOLLFIRKSPITICLVLDLAPSKGTVNLTWASASGKPVNHSTRKEEKORNGTLTVST 424
DB	224 PSFOLLFIRKSPITICLVLDLAPSKGTVNLTWASASGKPVNHSTRKEEKORNGTLTVST 283
QY	425 LPVGTEDMTGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484
DB	284 LPVGTEDMTGETYQCRVTHPHLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343
QY	485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLVTRAWEQKDF 544
DB	344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKSGGFFVFSRLVTRAWEQKDF 403
QY	545 ICRVHAAASPSQTQVORAVSNVPGK 569
DB	404 ICRVHAAASPSQTQVORAVSNVPGK 428
RESULT 9	
AAM50940	
ID	AAM50940 standard; protein; 428 AA.
XX	
AC	AAM50940;
XX	
DT	15-MAY-2002 (first entry)
XX	
DE	Human IgE epsilon chain constant region.

QY	245	GGGSGFTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	304	CC	graft versus host disease and transplant rejection and/or allergic
Db	106	--SRDFTPTVKILQSSCDGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	163	CC	disease such as food allergy, hay fever, allergic rhinitis, allergic
QY	305	STTQEGELASTQSELTLISQKHLSDRITYTCQVYQGHFTPEDSTKKCADSNPRGVSAIYLSR	364	CC	asthma and venom allergy. The invention is also useful in cell therapy.
Db	164	STTQEGELASTQSELTLISQKHLSDRITYTCQVYQGHFTPEDSTKKCADSNPRGVSAIYLSR	223	CC	The present sequence is human immunoglobulin E (IgE) constant region.
QY	365	PSPDFLPIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTWST	424	CC	This protein is used in the exemplification of the invention. Note: This
Db	224	PSPDFLPIRKSPITITCLVVDLAPSKGTVNLTSRASGKPVNHSRKEEKORNGTLTWST	283	CC	sequence is stated to be the same as that shown in figure 10 (AAB35114)
QY	425	LPVGTREDWIEGETYQCRVTHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTL	484	CC	of the specification. However these sequences differ
Db	284	LPVGTREDWIEGETYQCRVTHPHLPRALMRSTTKSGPRAAPEVYAFATPEWPGSRDKRTL	343	XX	
QY	485	ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVTRAWEQKDEF	544	QY	Sequence 428 AA;
Db	344	ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLVTRAWEQKDEF	403	Query Match	57.7%; Score 1766; DB 6; Length 428;
QY	545	ICRAVHEAASPSQTVORAVSNPGK 569		Best Local Similarity	78.0%; Pred. No. 1.6e-113;
Db	404	ICRAVHEAASPSQTVORAVSNPGK 428		Matches	347; Conservative 17; Mismatches 57; Indels 24; Gaps 7;
RESULT 10					
AAE35113					
ID	AAE35113	standard; protein; 428 AA.			
XX	AAE35113;				
XX	28-MAY-2003	(first entry)			
DE	Human immunoglobulin E (IgE) constant region.				
KW	Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy;				
KW	lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis;				
KW	psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever;				
KW	inflammatory bowel disease; insulin dependent diabetes; cell therapy;				
KW	Crohn's disease; allergic rhinitis; graft versus host disease; asthma;				
XX	transplant rejection; human; immunoglobulin E; IgE.				
OS	Homo sapiens.				
XX	WO200292773-A2.				
PD	21-NOV-2002.				
XX	13-MAY-2002; 2002WO-US015341.				
XX	15-MAY-2001; 2001US-0291300P.				
PA	(ORTH ) ORTHO-MCNEIL PHARM INC.				
PI	Cai Z, Jackson MR, Peterson PA, Shi W, Kong Y, Degraw J;				
XX	WPI; 2003-120673/11.				
PT	Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases,				
PT	comprises culturing CD8+ T cells with antigen presenting cells to				
PT	activate precursor CD8+ T cells specific for T the cell epitopes.				
PS	Disclosure; Fig 7; 49pp; English.				
CC	The invention relates to a method of producing cytotoxic T lymphocytes				
CC	(CTLs) specific for one or more non-tumour self antigen T cell epitopes.				
CC	The method involves loading antigen presenting cells (APCs) having class				
CC	I major histocompatibility complex molecules with the T cell epitopes, T				
CC	cells specific for the CD8+ T cells with the APCs to activate precursor CD8+ T				
CC	cells specific for the T cell epitopes. The invention is useful for				
CC	treating autoimmune disease including rheumatoid arthritis, psoriasis,				
CC	lupus, autoimmune nephritis, multiple sclerosis, autoimmune thyroiditis,				
CC	insulin dependent diabetes, Crohn's disease, inflammatory bowel disease,				





Db 63 SGHYATISLTV-SGAWAK-QMTICRVAHTPSSDWDVNDKTFVUC----- 105  
QY 245 GGGGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 304  
Db 106 --SRDFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQVMDVLDSTA 163  
QY 305 STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSR 364  
Db 164 STTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPRGVSAYLSR 223  
QY 365 PSPFDLPIRKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORNGTLTWST 424  
Db 224 PSPFDLPIRKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORNGTLTWST 283  
QY 425 LPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 484  
Db 284 LPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTL 343  
QY 485 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLEVTRAEBWQKDEF 544  
Db 344 ACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLEVTRAEBWQKDEF 403  
QY 545 ICRAVHEAASPSTQVQRAVSNPGK 569  
Db 404 ICRAVHEAASPSTQVQRAVSNPGK 428  
  
RESULT 14  
AAP40065  
ID AAP40065 standard; protein; 493 AA.  
XX AAP40065;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-FEB-1992 (first entry)  
DE Sequence of human immunoglobulin E H-chain.  
XX  
KW Antibody; allergy suppressor; immunological.  
OS Homo sapiens.  
XX  
PN EP102634-A.  
XX  
PD 14-MAR-1984.  
XX  
XX 03-SEP-1983; 83EP-00108699.  
PF  
XX  
PR 07-SEP-1982; 82JP-00156285.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Kikuchi M, Kurokawa T, Onda H;  
XX  
XX WPI; 1984-070437/12.  
DR N-PSDB; AAN40062.  
XX  
XX Polypeptide having activity of human immunoglobulin E - prep'd. from host  
PT transformed with recombinant DNA.  
XX  
XX Disclosure; Fig 2; 61pp; English.  
XX  
CC DNA encoding IgE H-chain and frags. is claimed (AAN40062). Transformant  
CC contg. the DNA is also new, esp. Escherichia coli IFO- 14284, -5 and -6.  
CC The transformant may be grown to produce a polypeptide of immunological  
CC or biological activity equivalent to that of the human IgE H chain.  
CC AAN40062 or frags. is pref. linked at a site downstream from a promoter,  
CC e.g. rec A promoter (see AAN40064). (Updated on 25-MAR-2003 to correct PA  
XX field.)  
XX Sequence 493 AA;

Query Match 57.5%; Score 1760; DB 1; Length 493;  
Best Local Similarity 77.0%; Pred. No. 5e-113;  
Matches 349; Conservative 14; Mismatches 66; Indels 24; Gaps 7;  
  
QY 120 TISKAKVQPREPOVYTLPPSRDELTKNQVSLT--CLVKGFPSPDIAVEWESNQPENNYK 177  
Db 62 TVSSASTQ--SRSVFPLTRCCKNIPSNATSVTLGCLATGYFPEPVMVTDWT-GSLNGTMM 118  
QY 178 TTP-PVLDSVGGFFLYSLKLTVDKSRWQQGNVFSQSVMEALHNHYQORSLSLSPGKVEGG 236  
Db 119 TLPATTLTSLGHYATISLTV-SGAWAK-QIETCRVAHTPSSDWDVNDKTF----- 167  
QY 237 GSGGGGGGGGSGFTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQV 296  
Db 168 -----SVCSRDFPTPTVKILQSSCDGGGHPPTIQLLCLVSGYTPGTINITWLEDQV 220  
QY 297 MDVDLSTASTTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPR 356  
Db 221 MDVDLSTASTTQEGELASTQSELTLQSKHWSLDRYTCQVYQGHFTFEDSTKKCADSNPR 280  
QY 357 GVSAYLSRSPDLPFRKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORN 416  
Db 281 GVSAYLSRSPDLPFRKSPITITCLVVDLAPSKGTVNLTWASRGKPVNHSRKEEKORN 340  
QY 417 GTLTVTSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKTSGPRAAPEVYAFATPEW 476  
Db 341 GTLTVTSTLPVGTDRWIEGETYQCRVTHPHPLPALMRSTTKTSGPRAAPEVYAFATPEW 400  
QY 477 GSRDKRTLACLQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLEVTRA 536  
Db 401 GSRDKRTLACLQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTGSGFFVFSRLEVTRA 460  
QY 537 EWEQKDEFICRAVHEAASPSTQVQRAVSNPGK 569  
Db 461 EWEQKDEFICRAVHEAASPSTQVQRAVSNPGK 493  
  
RESULT 14  
AAU80287  
ID AAU80287 standard; protein; 441 AA.  
XX AAU80287;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Human IgE heavy chain C1-C2-C3-C4 domains with MIGIS fragment.  
XX  
KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;  
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
KW heavy chain C domain; MIGIS.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
PH Key Location/Qualifiers  
FT Domain 11..106  
FT /notes= "IgE heavy chain C1 domain"  
FT Domain 113..208  
FT /label= IgE heavy chain C2 domain  
FT Region 205..219  
FT /notes= "Epitope including C2C3 linker"  
FT Region 209..216  
FT /notes= "Linker domain between C2 and C3 region"  
FT Domain 217..317  
FT /notes= "IgE heavy chain C3 domain"  
FT Region 244..251  
FT /notes= "Epitope in BC loop"  
FT Region 244..251  
FT /notes= "Epitope in BC loop"  
FT Region 272..280  
FT /notes= "Epitope in DE loop"  
FT Region 301..311





CC or lyophilized form of target Ig derived protein; and a method for  
CC producing an isolated mammalian target Ig derived protein. The target Ig  
CC derived protein is useful in preparing a composition for diagnosing or  
CC treating a target related condition in a cell, tissue, organ or animal,  
CC e.g. tumor. This is the amino acid sequence of variable heavy chain  
CC region Igs. Note: This sequence differs from the version given in SEQ ID  
CC NO 35 in which the X residues have not been expanded to represent the  
CC whole CDR regions.  
XX  
XX  
SQ Sequence 497 AA;

Query Match	57.3%;	Score 1754.5;	DB 9;	Length 497;
Best Local Similarity	77.5%;	Pred. No. 1.2e-112;		
Matches 347;	Conservative 17;	Mismatches 57;	Indels 27;	Gaps 8;
Qy	129	REPQVYTLPPSRDELTKNQVSLT--CLVKGFPYPSDIAVEWESNGQPENNYKTPP-PVLDS	185	
Db	4	QSPSVFPLTRCCCKNIPSNATSVTLGCLATGYFPEPVMTWDT-GSLNGTTMTLPATTLTL	62	
Qy	186	VGSFFLYSKLTVDKSRQCNVFCSCVMHEALHNHY-QQRSLSLSPCKVEGGGGGGGS	244	
Db	63	SGHYATISLLTV-SGAWAK-QMFTCRVAHPSTDMVDNKTFSVC-----	105	
Qy	245	GGGSGFTPTPVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	304	
Db	106	--SRDFTPTPVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDQVMDVDLSTA	163	
Qy	305	STTQEGELASTQSELTLISQKHMLSRTYTCQVYQGHTEPDKKCADSNPRGVSYLSR	364	
Db	164	STTQEGELASTQSELTLISQKHMLSRTYTCQVYQGHTEPDKKCADSNPRGVSYLSR	223	
Qy	365	PSPPDLPIRKSPTITCLVVDLAPSKGVNLTWSRASKPVNHSRKEEKORNGTLTVTST	424	
Db	224	PSPPDLPIRKSPTITCLVVDLAPSKGVNLTWSRASKPVNHSRKEEKORNGTLTVTST	283	
Qy	425	LPVGTDRWIEGETYQCRVTHPHLPALMRSTTKTS---GPRAAPEVYAFATPEWPGSRDK	481	
Db	284	LPVGTDRWIEGETYQCRVTHPHLPALMRSTTKTS---GPRAAPEVYAFATPEWPGSRDK	343	
Qy	482	RTLACLIONPMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVFSRLLEVTRAWEQK	541	
Db	344	RTLACLIONPMPEDISVQWLHNEVQLPDARHSTTPQPKTKGSGFFVFSRLLEVTRAWEQK	403	
Qy	542	DEFICRAVHEAASPSQTVQRAVSNPCK	569	
Db	404	DEFICRAVHEAASPSQTVQRAVSNPCK	431	

Search completed: November 30, 2005, 00:28:31  
Job time : 192 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:16:42 ; Search time 42 seconds  
(without alignments)

1303.508 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHCPCPAPELL.....HEAAPSQTQRAVSNVPGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1766	57.7	428	1 EHHU	Ig epsilon chain C
2	1705.5	55.7	426	2 I36948	Ig epsilon-chain -
3	1225	40.0	330	1 GHU	Ig gamma-1 chain C
4	1219	39.8	374	2 S69339	Ig heavy chain V r
5	1217	39.8	255	4 S31866	Ig gamma-1 chain C
6	1172	38.3	234	2 PT0207	Ig gamma chain C r
7	1138	37.2	377	2 A23511	Ig gamma-3 chain C
8	1136	37.1	377	2 A60764	Ig gamma-3 chain C
9	1123	36.7	289	1 G3HUW1	Ig gamma-3 heavy C
10	1107	36.2	326	1 G2HU	Ig gamma-2 chain C
11	1097	35.8	327	1 G4HU	Ig gamma-4 chain C
12	883	28.9	323	1 GHRB	Ig gamma chain C r
13	868.5	28.4	328	2 I47160	Ig gamma 2b chain
14	868.5	28.4	328	2 I47159	Ig gamma 2a chain
15	865	28.3	327	2 I47162	Ig gamma 4 chain c
16	862.5	28.2	429	1 EHT	Ig epsilon chain C
17	858	28.0	329	1 G2GP	Ig gamma-2 chain C
18	847.5	27.7	328	2 I47158	Ig gamma 1 chain c
19	840.5	27.5	328	2 I47161	Ig gamma 3 chain c
20	834.5	27.3	548	2 S38864	Ig epsilon chain C
21	820	26.8	470	2 S22080	Ig heavy chain pre
22	813	26.6	333	2 PS0018	Ig gamma-2b chain
23	812.5	26.6	329	1 G3MSC	Ig gamma-3 chain C
24	811.5	26.5	308	2 C30554	Ig heavy chain C r
25	811.5	26.5	472	2 S31459	Ig gamma-1 chain -
26	801.5	26.2	398	1 G3MSM	Ig gamma-3 chain C
27	794.5	26.0	444	2 PC4436	monoclonal antibod
28	789.5	25.8	324	1 GLMS	Ig gamma-1 chain C
29	784.5	25.6	326	2 PS0017	Ig gamma-1 chain C

RESULT 1

EHHU

Ig epsilon chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 09-Jul-2004

C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46

R;Flanagan, J.G.; Rabbitts, T.H.

EMBO J. 1, 655-660, 1982

A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene

A;Reference number: A22771; MUID:84236029; PMID:6234164

A;Accession: A22771

A;Molecule type: DNA

A;Residues: 1-428 <FLA>

A;Cross-references: UNIPROT:P01854; UNIPARC:UPI000004BB48; GB:L00022; GB:J00227; GB:V005

R;Ueda, S.; Nakai, S.; Mishida, Y.; Hisajima, H.; Honjo, T.

EMBO J. 1, 1539-1544, 1982

A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog

A;Reference number: A23195; MUID:84207910; PMID:6327276

A;Accession: A23195

A;Molecule type: DNA

A;Residues: 2-428 <UED>

A;Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:gl84755

R;Zhang, K.; Saxon, A.; Max, E.E.

J. Exp. Med. 176, 233-243, 1992

A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing

A;Reference number: PH1214; MUID:92308839; PMID:1613458

A;Accession: PH1214

A;Molecule type: DNA

A;Residues: 320-428 <ZHA>

A;Cross-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S38668; NID:G32987

R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Saeada, R.; Igarashi, K.; Kikuchi, M.; Sugf

Nucleic Acids Res. 11, 719-726, 1983

A;Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha

A;Reference number: A93491; MUID:83168897; PMID:6300763

A;Accession: A93491

A;Molecule type: mRNA

A;Residues: 1-428 <SEN>

A;Cross-references: UNIPARC:UPI000004BB48; GB:L00022; GB:J00227; GB:V00555; NID:gl85035

R;Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.

Cell 29, 691-699, 1982

A;Title: Duplication and deletion in the human immunoglobulin epsilon genes.

A;Reference number: A90824; MUID:83001945; PMID:6288268

A;Accession: A90824

A;Molecule type: DNA

A;Residues: 1-358, 'L', 360-428 <MAX>

A;Cross-references: UNIPARC:UPI0000173784; GB:J00222; NID:gl84755

A;Note: this sequence difference may be due to polymorphism

R;Pennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.

in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-1

A;Reference number: A94418

A;Accession: A94418

A;Molecule type: protein



QY 305 STTOGELASTQSELTLSOKHLSDRTVTCOVYQGHTEFSTKKCADSNPRGVSAYLSR 364  
Db 162 SATOGEELASTQSELTLSOKHLSDRTVTCOVYQGHTEFSTKKCADSNPRGVSAYLSR 221  
QY 365 PSPFDLFRKSPPTITCLVVDLAPSKGVNLTWSRASGKPVNHSRKEEKORNGTLTVTST 424  
Db 222 PSPFDLFRKSPPTITCLVVDLAPSKGVNLTWSRASGKPVNHSRKEEKORNGTLTVTST 281  
QY 425 LPVGTROWIEGTQCRVTHPHLPRALMRSTTKSGPRAAEVYAFATPEWPGSRDKRTL 484  
Db 282 LPVGTROWIEGTQCRVTHPHLPRALMRSTTKSGPRAAEVYAFATPEWPGSRDKRTL 341  
QY 485 ACLIQNFWPEDISVQWLHNEVQLDARHSTTQPKTKGSGFFVFSRLLEVTRAWEQKDEF 544  
Db 342 ACLIQNFWPEDISVQWLHNEVQLDARHSTTQPKTKGSGFFVFSRLLEVTRAWEQKDEF 401  
QY 545 ICRAVHEAASPQTQVRAVSVPNGK 569  
Db 402 ICRAVHEAASPQTQVRAVSVPNGK 426  
RESULT 3  
GHU  
Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034COE; EMBL:Z17370  
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,  
A:Note: Lys-330 is removed after translation  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S33904  
A:Accession: S36861  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:Cross-references: UNIPARC:UPI000013CGFE; EMBL:Z17370  
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; MUID:83001943; PMID:6811139  
A:Accession: S33887  
A:Molecule type: DNA  
A:Residues: 88-113;235-330 <TAK>  
A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370  
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,  
Biochemistry 9, 3161-3170, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A:Reference number: A90563; MUID:71064024; PMID:5489771  
A:Contents: myeloma protein Eu  
A:Accession: B90563  
A:Molecule type: protein  
A:Residues: 1-96, R', 98-135 <CUN>  
A:Cross-references: UNIPARC:UPI000017378D  
A:Note: this sequence has the G1m(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen  
A:Reference number: A90564; MUID:71064025; PMID:5530842  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,  
A:Cross-references: UNIPARC:UPI000017378E  
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)  
igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 273-330 <H  
A:Cross-references: UNIPARC:UPI000017378F  
A:Note: this sequence has the G1m(17) and G1m(1) markers  
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 Ko1  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein Ko1; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A:Cross-references: UNIPARC:UPI0000173790  
A:Note: this sequence has the G1m(3) and G1m(non-1) markers  
R;Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 14  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83 144-204 250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 40.0%; Score 1225; DB 1; Length 330;  
Best Local Similarity 97.0%; Pred. No. 9.6e-69;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158  
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQWMNCKEYCKVSNKALPAPIKT 120  
Db 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIKT 218  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKPTP 180  
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKPTP 278  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCSCVMHEALHNHYTQKSLSLSPGK 232  
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCSCVMHEALHNHYTQKSLSLSPGK 330  
RESULT 4  
S69339  
Ig heavy chain V region precursor - human

C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C;Accession: S69339; S72664  
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A;Reference number: S69339; MUID:95262687; PMID:7744049  
A;Accession: S69339  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <KHA>  
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695  
R;Khamlichi, A.A.  
submitted to the EMBL Data Library, September 1994  
A;Reference number: S72664  
A;Accession: S72664  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140, 'C', 142-374 <KH2>  
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695  
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 39.8%; Score 1219; DB 2; Length 374;  
Best Local Similarity 96.1%; Pred. No. 2.6e-68;  
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 143 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 203 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 262  
QY 121 ISKAKVQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 263 ISKAKGQPREPOVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 322  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
DB 323 PVLDSGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 374

RESULT 5  
S31866  
Ig gamma-1 chain C region - synthetic  
C;Species: synthetic  
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C;Accession: S31866  
R;Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A;Description: Screening method for protein-protein interactions of cloned gene products.  
A;Reference number: S31866  
A;Accession: S31866  
A;Molecule type: mRNA  
A;Residues: 1-255 <FIL>  
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID  
F;1-22/Region: Escherichia coli outer membrane protein A precursor  
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 39.8%; Score 1217; DB 4; Length 255;  
Best Local Similarity 96.6%; Pred. No. 2.2e-68;  
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 24 ESKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 84 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 143

QY 121 ISKAKVQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 144 ISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 203  
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
DB 204 PVLDSGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 255

RESULT 6

PT0207  
Ig gamma chain C region - chimpanzee  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C;Accession: PT0207  
R;Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A;Reference number: PT0207; MUID:91287716; PMID:2062315  
A;Accession: PT0207  
A;Molecule type: mRNA  
A;Residues: 1-234 <EHR>  
A;Cross-references: UNIPARC:UPI0000176F05  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;48-117/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 1172; DB 2; Length 234;  
Best Local Similarity 95.6%; Pred. No. 1.2e-65;  
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 10 EPKSCDTHTTTPCAAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 69  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120  
DB 70 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 129  
QY 121 ISKAKVQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 130 ISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 189

RESULT 7

A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C;Accession: A23511  
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: con  
A;Reference number: A23511; MUID:86148507; PMID:3081877  
A;Accession: A23511  
A;Molecule type: DNA  
A;Residues: 1-377 <HUC>  
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272  
C;Genetics:  
A;Gene: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 14q32.33-14q32.33  
C;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMW>

Query Match 37.2%; Score 1138; DB 2; Length 377;

```

Best Local Similarity 89.7%; Pred. No. 2.8e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 60
Db 146 EPKSCDTPPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 205
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLQHWNNMGKEVKCKVSNKALPAPIEKT 120
Db 206 KWIYVDGVEVHNKTKPREEQNSTFRVSVLTVTLQHWNNMGKEVKCKVSNKALPAPIEKT 265
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 266 ISKTKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYTTP 325
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFVSMHEALHNHYQOQSLSLSPGK 232
Db 326 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFVSMHEALHNRYTQKSLSLSPGK 377

RESULT 8
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:CROSS-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 37.1%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 3.7e-63;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 60
Db 146 EPKSCDTPPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 205
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLQHWNNMGKEVKCKVSNKALPAPIEKT 120
Db 206 KWIYVDGVEVHNKTKPREEQNSTFRVSVLTVTLQHWNNMGKEVKCKVSNKALPAPIEKT 265
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 266 ISKTKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYTTP 325
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFVSMHEALHNHYQOQSLSLSPGK 232
Db 326 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFVSMHEALHNRYTQKSLSLSPGK 377

RESULT 9
G3HUM1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy
A:Reference number: A90442; MUID:81021548; PMID:677477
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein

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A:Residues: 1-289 <FRA>
A:CROSS-references: UNIPARC:UPI0000173797
A:Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A:Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 cc
R:Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A:Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A:Reference number: A92219; MUID:77118561; PMID:402363
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein Wis
A:Accession: A92219
A:Molecule type: protein
A:Residues: 12-97 <MIC>
A:CROSS-references: UNIPARC:UPI0000173798
A:Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A:Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R:Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A:Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A:Reference number: A90198; MUID:77021516; PMID:823945
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A:CROSS-references: UNIPARC:UPI0000173799
A:Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R:Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A:Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A:Reference number: A93915; MUID:82247835; PMID:6808505
A:Contents: heavy chain disease protein Omm
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A:CROSS-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C
A:Note: a carboxyl-terminal Lys is removed posttranslationally
A:Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:CROSS-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 36.7%; Score 1123; DB 1; Length 289;
Best Local Similarity 88.3%; Pred. No. 1.7e-62;
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 60
Db 59 EPKSCDTPPPCPAPPELLGGPSVFLPPKPKDMLSRTPETVTCVVVDVSHEDPEVKF 118
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVTLQHWNNMGKEVKCKVSNKALPAPIEKT 120
Db 119 KWIYVDGVEVHNKTKPREEQNSTFRVSVLTVTLQHWNNMGKEVKCKVSNKALPAPIEKT 178
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 179 ISKTKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYTTP 238
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFVSMHEALHNHYQOQSLSLSPG 231
Db 239 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCFVSMHEALHNRYTQKSLSLSPG 289

RESULT 10
G2HU
Ig gamma-2 chain C region - human

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C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6804948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:G32  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein Til  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A:Cross-references: UNIPARC:UPI0000173791  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of a  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793  
A:Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
A:Cross-references: UNIPARC:UPI0000173794  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati  
ned  
R:Wilstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMI>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.2%; Score 1107; DB 1; Length 326;  
Best Local Similarity 88.4%; Pred. No. 1.9e-61;  
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;  
QY 1 EPKSCDKTHTCCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 ERKCCVE---CPCCAPP-VAGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 154  
QY 61 NMYVDGVEVHNKTKPREQYNSTYRVSVLTFLHONMNGKEYCKVSKNKGALPAPIETK 120  
DB 155 NMYVDGVEVHNKTKPREQYNSTYRVSVLTFLHONMNGKEYCKVSKNKGALPAPIETK 214  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGQPNVKKTP 180  
DB 215 ISKTKQPREPOVYTLPPSRDEMTKNVSLTCLVKGFPSPDIATVWESNGQPNVKKTP 274  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNNHYTKSLSLSPGK 232  
DB 275 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNNHYTKSLSLSPGK 326  
RESULT 11  
G4HU  
IG gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104; PMID:6299662  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re  
A:Reference number: A90249; MUID:70207560; PMID:4192699  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796  
C:Genetics:  
A:Gene: GDB:IGHG4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMI>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted  
F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 35.8%; Score 1097; DB 1; Length 327;  
Best Local Similarity 90.5%; Pred. No. 8e-61;  
Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
QY 11 CPCCAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNVDGVEVH 70  
DB 106 CPSCPAPEFLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNVDGVEVH 165  
QY 71 NVKTKPREQYNSTYRVSVLTFLHONMNGKEYCKVSKNKGALPAPIETKISKAKVQPRE 130  
DB 166 NAKTKPREQYNSTYRVSVLTFLHONMNGKEYCKVSKNKGALPAPIETKISKAKVQPRE 225





A;Residues: 1-328 <KAC>  
A;Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PI  
C;Genetics:  
A;Gene: IGG2a  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 28.4%; Score 868.5; DB 2; Length 328;  
Best Local Similarity 70.1%; Pred. No. 1.1e-46;  
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

QY 11 CPPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70  
DB 106 CPICPACE-SPGPSVFIFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
QY 71 NVKTKPREQYNSTYRVVSVLTVLHQNWMMGKEYCKCKVSNKALPAPIEKTISKAKVQPRE 130  
DB 165 TAQTRPKEEQFNSTYRVVSVLPIQHODWLNGKEFKCKVNNKDLPAPIITRIISKAKGQTR 224  
QY 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDVSGS 188  
DB 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQNGQPEPEGNRYRTTPPQQDVGDT 284  
QY 189 FFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYQORSLSLSPGK 232  
DB 285 YFLYSKFSVDKASWQGGIGFQCAVMHEALHNHYTQKSISKTPGK 328

RESULT 15  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C;Accession: I47162  
R;Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A;Reference number: I47158; MUID:95015845; PMID:7930579  
A;Accession: I47162  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-277 <KAC>  
A;Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:G433129; PIDN:AAA52220.1; PI  
C;Genetics:  
A;Gene: IGG4  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 28.3%; Score 865; DB 2; Length 277;  
Best Local Similarity 69.0%; Pred. No. 1.15e-46;  
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;

QY 8 THTCPPCP-APPELLG-GPSVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65  
DB 49 TKTKPFCPCIPACEGPGPSAFIFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 108  
QY 66 GVEVHNVTKPREQYNSTYRVVSVLTVLHQNWMMGKEYCKCKVSNKALPAPIEKTISKAK 125  
DB 109 GVEVHTAQTREPKEEQFNSTYRVVSVLPIQHODWLNGKEFKCKVNNKDLPAPIITRIISKAK 168  
QY 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPV 183  
DB 169 GQTRPEQVYTLPPPTPELSRSKVTCLVTGYFPDIDVEWQNGQPEPEGNRYRTTPPQQ 228  
QY 184 DSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYQORSLSLSPGK 232  
DB 229 DVDGTITFLSKLAVDKASWQGGITFQCAVMHEALHNHYTQKSIFKTPGK 277

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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:15:42 ; Search time 229 Seconds

(without alignments)  
1753.038 Million cell updates/sec

Title: US-09-847-208B-7

Perfect score: 3060

Sequence: 1 EPKSCDKTHCPCPAPPELL.....HEAAPSQTVORAVSNPGK 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05\_80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1766	57.7	428	1 IGHE HUMAN	P01854 homo sapien
2	1225	40.0	330	1 IGHI HUMAN	P01857 homo sapien
3	1225	40.0	465	2 Q6GMX6 HUMAN	Q6gmx6 homo sapien
4	1225	40.0	466	2 Q6IN78 HUMAN	Q6in78 homo sapien
5	1225	40.0	469	2 Q569F4 HUMAN	Q569f4 homo sapien
6	1225	40.0	469	2 Q727P5 HUMAN	Q727p5 homo sapien
7	1225	40.0	470	2 Q725W1 HUMAN	Q725w1 homo sapien
8	1225	40.0	470	2 Q6PJA4 HUMAN	Q6pia4 homo sapien
9	1225	40.0	472	2 Q6N089 HUMAN	Q6n089 homo sapien
10	1225	40.0	475	2 Q5EFES HUMAN	Q5efes homo sapien
11	1225	40.0	475	2 Q6GMW7 HUMAN	Q6gmw7 homo sapien
12	1225	40.0	476	2 Q6GMX1 HUMAN	Q6gmx1 homo sapien
13	1225	40.0	679	2 Q6PQ08 HUMAN	Q6pq08 homo sapien
14	1221	39.9	473	2 Q6PQ05 HUMAN	Q6pq05 homo sapien
15	1221	39.9	475	2 Q6MZQ6 HUMAN	Q6mzq6 homo sapien
16	1221	39.9	480	2 Q6N094 HUMAN	Q6n094 homo sapien
17	1221	39.9	481	2 Q6N097 HUMAN	Q6n097 homo sapien
18	1221	39.9	482	2 Q72351 HUMAN	Q72351 homo sapien
19	1219	39.8	348	2 Q6FYX1 HUMAN	Q6fyx1 homo sapien
20	1219	39.8	473	2 Q6MZV7 HUMAN	Q6mzv7 homo sapien
21	1219	39.8	478	2 Q6P181 HUMAN	Q6p181 homo sapien
22	1219	39.8	480	2 Q6P1F1 HUMAN	Q6p1f1 homo sapien
23	1218	39.8	466	2 Q6N096 HUMAN	Q6n096 homo sapien
24	1214	39.7	475	2 Q6N095 HUMAN	Q6n095 homo sapien
25	1214	39.7	544	2 Q6PQ95 HUMAN	Q6pq95 homo sapien
26	1196	38.0	487	2 Q65ZL2 9MURI	Q65z12 mus sp. fv/
27	1164	38.1	487	2 Q5RE17 PONPY	Q5re17 pongo pygma
28	1138	37.2	354	2 Q6FTT2 HUMAN	Q6ftt2 homo sapien
29	1138	37.2	518	2 Q6N030 HUMAN	Q6n030 homo sapien
30	1138	37.2	519	2 Q5EBM2 HUMAN	Q5ebm2 homo sapien
31	1134	37.1	521	2 Q8N4Y9 HUMAN	Q8n4y9 homo sapien

RESULT 1				
IGHE HUMAN	STANDARD;	PRT;	428 AA.	
ID	IGHE HUMAN			
AC	P01854;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig epsilon chain C region.			
GN	Name=IGHE;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=83168897; PubMed=6300763;			
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,			
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;			
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin			
RT	epsilon chain cDNA.";			
RL	Nucleic Acids Res. 11:719-726(1983).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE, AND VARIANT LEU-359.			
RX	MEDLINE=83001945; PubMed=6288268; DOI=10.1016/0092-8674(82)90185-4;			
RA	Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;			
RT	"Duplication and deletion in the human immunoglobulin epsilon genes.";			
RL	Cell 29:691-699(1982).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=84236029; PubMed=6234164;			
RA	Planagan J.G., Rabbitts T.H.;			
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant			
RT	region gene, and evidence for three non-allelic genes.";			
RL	EMBO J. 1:655-660(1982).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=84207910; PubMed=6327276;			
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;			
RT	"Long terminal repeat-like elements flank a human immunoglobulin			
RT	epsilon pseudogene that lacks introns.";			
RL	EMBO J. 1:1539-1544(1982).			
RN	[5]			
RP	PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).			
RP	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;			
RA	(In) Bach M.K. (eds.);			
RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36,			
RL	Marcel Dekker, New York (1978).			
RN	[6]			
RP	NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428.			
RX	MEDLINE=83065234; PubMed=6815656;			
RA	Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,			
RA	Bell L.O., Gould H.J.;			
RT	"Cloning and sequence determination of the gene for the human			

P01860 homo sapien  
Q8nf17 homo sapien  
P01859 homo sapien  
Q6n093 homo sapien  
Q6mzu6 homo sapien  
Q6p624 homo sapien  
P01861 homo sapien  
Q8tc63 homo sapien  
Q68cn4 homo sapien  
Q6mzx7 homo sapien  
P01870 oryctolagus  
Q95m34 equus caball  
P01855 rattus norv  
P01862 cavia porce

## ALIGNMENTS



DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
CC [1]  
CC NUCLEOTIDE SEQUENCE.  
CC MEDLINE=92274238; PubMed=6287432;  
CC Ellison J.W.; Berson B.J.; Hood L.E.;  
CC "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
CC Nucleic Acids Res. 10:4071-4079(1982).  
CC [2]  
CC PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
CC MEDLINE=71064024; PubMed=5489771;  
CC Cunningham B.A.; Rutishauser U.; Gall W.E.; Gottlieb P.D.;  
CC Waxdal M.J.; Edelman G.M.;  
CC "The covalent structure of a human gamma G-immunoglobulin. VII. Amino  
CC acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
CC Biochemistry 9:3161-3170(1970).  
CC [3]  
CC PROTEIN SEQUENCE OF 136-329 (EU).  
CC MEDLINE=71064025; PubMed=5530842;  
CC Rutishauser U.; Cunningham B.A.; Bennett C.; Konigsberg W.H.;  
CC Edelman G.M.;  
CC "The covalent structure of a human gamma G-immunoglobulin. 8. Amino  
CC acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
CC Biochemistry 9:3171-3181(1970).  
CC [4]  
CC PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).  
CC MEDLINE=77070269; PubMed=826475;  
CC Ponstingl H.; Hilschmann N.;  
CC "The rule of antibody structure. The primary structure of a monoclonal  
CC IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic  
CC peptides of the H-chain, alignment of the tryptic peptides and  
CC discussion of the complete structure.";  
CC Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
CC [5]  
CC PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
CC MEDLINE=83289131; PubMed=6884994;  
CC Schmidt W.E.; Jung H.-D.; Palm W.; Hilschmann N.;  
CC "Three-dimensional structure determination of antibodies. Primary  
CC structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
CC Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
CC [6]  
CC DISULFIDE BONDS.  
CC MEDLINE=71064027; PubMed=4923144;  
CC Gall W.E.; Edelman G.M.;  
CC "The covalent structure of a human gamma G-immunoglobulin. X.  
CC Intrachain disulfide bonds";  
CC Biochemistry 9:3188-3196(1970).  
CC [7]  
CC DISULFIDE BONDS.  
CC MEDLINE=77070267; PubMed=1002129;  
CC Dreker L.; Schwarz J.; Reichel W.; Hilschmann N.;  
CC "Rule of antibody structure. The primary structure of a monoclonal  
CC IgG1 immunoglobulin (myeloma protein NIE), I: purification and  
CC characterization of the protein, the L- and H-chains, the cyanogen  
CC bromide cleavage products, and the disulfide bridges.";  
CC Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
CC [8]  
CC X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
CC MEDLINE=81208100; PubMed=7236608;  
CC Deisenhofer J.;  
CC "Crystallographic refinement and atomic models of a human Fc fragment  
CC and its complex with fragment B of protein A from Staphylococcus  
CC aureus at 2.9- and 2.8-A resolution.";  
CC Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: NIE has the G1M(17) allotypic marker, 97-K, and the

CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the  
CC G1M(3) marker and the G1M (non-1) markers.  
CC -!- MISCELLANEOUS: NIE also differs in the amidation states of 35,  
CC 116, 198, 269 and 272.  
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; J00228; AAC82527.1; ALT\_INIT; Genomic\_DNA.  
CC PIR; A93433; GHHU.  
CC PDB; 1AJ7; X-ray; H=1-103.  
CC PDB; 1AQK; X-ray; H=1-103.  
CC PDB; 1D5B; X-ray; B/H=1-101.  
CC PDB; 1D51; X-ray; H=1-101.  
CC PDB; 1D6V; X-ray; H=1-101.  
CC PDB; 1DN2; X-ray; A/B=120-326.  
CC PDB; 1E4K; X-ray; A/B=106-330.  
CC PDB; 1FC1; X-ray; A/B=106-329.  
CC PDB; 1FC2; X-ray; D=106-329.  
CC PDB; 1FCC; X-ray; A=121-326.  
CC PDB; 1H2H; X-ray; H/K=1-330.  
CC PDB; 1H7Z; X-ray; B/D=1-103.  
CC PDB; 1IIS; X-ray; A/B=107-330.  
CC PDB; 1IIX; X-ray; A/B=107-330.  
CC PDB; 1L6X; X-ray; A=120-326.  
CC PDB; 1QQX; X-ray; A/B=119-330.  
CC PDB; 1T83; X-ray; A/B=107-330.  
CC PDB; 2RCS; X-ray; H=1-103.  
CC HGNC; HGNC:5525; IGHG1.  
CC MIM; 147100; .  
CC GO; GO:0005624; C:membrane fraction; NAS.  
CC GO; GO:0003823; F:antigen binding; TAS.  
CC GO; GO:0006955; P:immune response; NAS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003597; Ig cl.  
CC InterPro; IPR003006; Ig\_MHC.  
CC Pfam; PF07654; CI-set; 3.  
CC PROSITE; PS00835; IG\_LIKE; 3.  
CC PROSITE; PS00290; IG\_MHC; 2.  
CC 3D-structure; Direct protein sequencing; Glycoprotein;  
CC Immunoglobulin C region; Immunoglobulin domain.  
CC REGION 1 98  
CC REGION 99 110 Hinge.  
CC REGION 111 223 CH2.  
CC REGION 224 330 CH3.  
CC CARBOHYD 180 180 N-linked (GlcNAc...).  
CC DISULFID 27 83  
CC DISULFID 103 103 Interchain (with light chain).  
CC DISULFID 109 109 Interchain (with heavy chain).  
CC DISULFID 112 112 Interchain (with heavy chain).  
CC DISULFID 144 204  
CC DISULFID 250 308  
CC VARIANT 97 97  
CC  
CC VARIANT 239 239 K -> R (in G1M(3) marker).  
CC  
CC VARIANT 241 241 /FTID=VAR\_003886.  
CC  
CC NON\_TER 1 1 D -> E (in G1M(non-1) marker).  
CC STRAND 23 24 /FTID=VAR\_003887.  
CC STRAND 26 33 L -> M (in G1M(non-1) marker).  
CC STRAND 38 38 /FTID=VAR\_003888.  
CC STRAND 41 41  
CC TURN 42 45  
CC TURN 48 49

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FT STRAND 50 52
FT STRAND 57 58
FT TURN 59 61
FT STRAND 62 71
FT HELIX 73 75
FT TURN 76 78
FT STRAND 82 87
FT TURN 88 91
FT STRAND 92 97
FT TURN 102 103
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 149
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FT TURN 163 164
FT STRAND 165 167
FT STRAND 171 172
FT STRAND 176 177
FT TURN 179 180
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FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
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FT HELIX 238 242
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FT STRAND 261 266
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FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 311
FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 40.0%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 1e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWTVDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
Db 159 NWTVDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQWLNKNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
QY 181 PVLDSVGSFFLYSKLTVDSRWQOGNVFSCSVMHAEALHHYQORSLSLSPGK 232
Db 279 PVLDSVGSFFLYSKLTVDSRWQOGNVFSCSVMHAEALHHYQORSLSLSPGK 330

RESULT 3
Q6GMX6_HUMAN
ID Q6GMX6_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -: mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
KW SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
SQ

Query Match 40.0%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 234 EPKSCDKHTCCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293
QY 61 NWTVDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
Db 294 NWTVDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQWLNKNGKEYCKVSNKALPAPIEKT 353
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 354 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 413
QY 181 PVLDSVGSFFLYSKLTVDSRWQOGNVFSCSVMHAEALHHYQORSLSLSPGK 232
Db 414 PVLDSVGSFFLYSKLTVDSRWQOGNVFSCSVMHAEALHHYQORSLSLSPGK 465

RESULT 4

```

Q6IN78 HUMAN  
ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.  
AC Q6IN78; 2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE IGHI1 protein.  
GN Name=IGHI1;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Peripheral Nervous System;  
RG NIH MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC072419; AAH72419.1; -; mRNA.  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig.c1.  
DR InterPro; IPR003006; Ig.MHC.  
DR InterPro; IPR003596; Ig.v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCDEB81076E CRC64;  
Query Match 40.0%; Score 1225; DB 2; Length 466;  
Best Local Similarity 97.0%; Pred. No. 1.6e-74;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCTCPCPAPPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 235 EPKSCDKTHCTCPCPAPPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 294  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKYKSNKALPAPIEKT 120  
DB 295 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKYKSNKALPAPIEKT 354  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 355 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 414

181 PVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGK 232  
181 PVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGK 466  
RESULT 5  
QY Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.  
ID Q569F4 HUMAN PRELIMINARY; PRT; 469 AA.  
AC Q569F4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE IGH1 protein.  
GN Name=IGH1;  
OS Homo sapiens (Human)  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC092518; AAH92518.1; -; mRNA.  
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;  
Query Match 40.0%; Score 1225; DB 2; Length 469;  
Best Local Similarity 97.0%; Pred. No. 1.6e-74;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHCTCPCPAPPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 238 EPKSCDKTHCTCPCPAPPELLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297  
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKYKSNKALPAPIEKT 120  
DB 298 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKYKSNKALPAPIEKT 357  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 358 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 417  
QY 181 PVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGK 232  
418 PVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQQRSLSPGK 469  
RESULT 6

Q7Z7P5 HUMAN		
ID	Q7Z7P5_HUMAN PRELIMINARY;	PRT; 469 AA.
AC	Q7Z7P5;	
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	IGHG1 protein.	
GN	Names:IGHG1;	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]_TaxID=9606;	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Spleen;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Abarnson R.D., Mullahy S.J.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,	
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Spleen;	
RG	NIH MGC Project;	
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC051328; AAH51328.1; -; mRNA.	
DR	HSSP; P01857; 1HZH.	
DR	SMR; Q7Z7P5; 20-469.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig_c1.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF07654; C1-set; 3.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG_LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.	
KW	Immunoglobulin domain	
SQ	SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;	
Query Match		40.0%; Score 1225; DB 2; Length 469;
Best Local Similarity		97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative		3; Mismatches 4; Indels 0; Gaps 0;
QY	1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	238 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	297
QY	61 NWYVDGVEVHNVTKPREQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT	120
Db	298 NWYVDGVEVHNVTKPREQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT	357
QY	121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180
Db	358 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	417
QY	181 PVLDSGVSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK	232
Query Match		40.0%; Score 1225; DB 2; Length 470;
Best Local Similarity		97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative		3; Mismatches 4; Indels 0; Gaps 0;
QY	1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60
Db	239 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	298
QY	61 NWYVDGVEVHNVTKPREQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT	120
Db	299 NWYVDGVEVHNVTKPREQYNSTYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT	358
QY	121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180



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Db 359 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP 418
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYQOQSLSLSPGK 232
Db 419 PVLDSGDSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 470

RESULT 8
Q6PJA4 HUMAN
ID Q6PJA4 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulliahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Smerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; 1ADO.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 239 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 298

RESULT 9
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 472;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 241 EPKSCDKTHCTCPCPAPPELLGPGSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 300

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQNMNGKEYCKVKSNKALPAPIEKT 120
Db 301 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVHLQNMNGKEYCKVKSNKALPAPIEKT 360

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP 180
Db 361 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKPTTP 420

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYQOQSLSLSPGK 232
Db 421 PVLDSGDSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 472

RESULT 10
```

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Q5BFE5_HUMAN
ID Q5BFE5_HUMAN PRELIMINARY; PRT; 475 AA.
DC Q5BFE5
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Anti-Rhd monoclonal T125 gamma1 heavy chain precursor.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RL antibody T125.";
RL EMBL: AY894992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL. 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gamma1 heavy
FT CHAIN chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
DB 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 423
QY 181 PVLDVSGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 424 PVLDSDGSGFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 11
Q6GMW7_HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE5D736860F8 CRC64;

Query Match 40.0%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 1.6e-74;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
DB 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 423
QY 181 PVLDVSGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 424 PVLDSDGSGFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 475

RESULT 12
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ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Homo sapiens (human).
RP NUCLEOTIDE SEQUENCE.
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Db 508 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 567
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 568 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 627
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVNMHEALHNHYQOQSLSLSPGK 232
Db 628 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVNMHEALHNHYQOQSLSLSPGK 679

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ID Q6P055_HUMAN PRELIMINARY; PRT; 473 AA.
AC Q6P055
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;
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Query Match 39.9%; Score 1221; DB 2; Length 473;
Best Local Similarity 96.6%; Pred. No. 3e-74;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Db 242 EPKSCDKTHTCCPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 301
Qy 61 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120
Db 302 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 361
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180
Db 362 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 421
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSQVNMHEALHNHYQOQSLSLSPGK 232
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RESULT 15
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ID Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weill B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 39.9%; Score 1221; DB 2; Length 475;
Best Local Similarity 96.6%; Pred. No. 3.1e-74;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 244 EPKSCDKTHTCCPCAPPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 303
Qy 61 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT 120
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Db 364 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 423  
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Job time : 232 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 30, 2005, 00:25:23 ; Search time 45 seconds  
(without alignments)  
1045.388 Million cell updates/sec

Title: US-09-847-208B-7  
Perfect score: 3060  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/H COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707	55.8	331	2	US-09-401-636-1
2	1701	55.6	325	2	US-09-701-623C-1
3	1273.5	41.6	711	2	US-09-485-737B-90
4	1273.5	41.6	711	2	US-10-071-485-90
5	1247	40.8	277	2	US-09-428-082B-22
6	1243	40.6	268	2	US-09-428-082B-8
7	1243	40.6	269	2	US-09-422-838C-46
8	1232	40.3	660	2	US-09-181-706-8
9	1232	40.3	660	2	US-09-458-791-8
10	1232	40.3	660	2	US-09-459-066-8
11	1232	40.3	660	2	US-09-459-065-8
12	1229	40.2	379	2	US-10-679-999-9
13	1226	40.1	253	2	US-09-428-082B-16
14	1225	40.0	232	1	US-08-595-043A-50
15	1225	40.0	232	2	US-09-968-362A-26
16	1225	40.0	232	2	US-09-932-812A-26
17	1225	40.0	331	2	US-09-178-869-2
18	1225	40.0	331	2	US-09-761-413-2
19	1225	40.0	360	2	US-09-180-100-11
20	1225	40.0	360	2	US-09-949-713-11
21	1225	40.0	371	1	US-08-236-311-7
22	1225	40.0	371	2	US-08-457-918-7
23	1225	40.0	371	2	US-10-157-408-7
24	1225	40.0	376	2	US-09-180-100-22
25	1225	40.0	376	2	US-09-949-713-22
26	1225	40.0	396	1	US-08-784-512-3
27	1225	40.0	396	2	US-09-176-228-3

28	1225	40.0	424	4	PCT-US95-03866-12	Sequence 12, Appl
29	1225	40.0	424	4	PCT-US95-03866-14	Sequence 14, Appl
30	1225	40.0	437	4	PCT-US96-10043-11	Sequence 11, Appl
31	1225	40.0	442	2	US-08-472-888A-7	Sequence 7, Appl
32	1225	40.0	442	2	PCT-US96-10043-9	Sequence 9, Appl
33	1225	40.0	446	2	US-08-397-411-7	Sequence 7, Appl
34	1225	40.0	449	1	US-08-458-516-13	Sequence 13, Appl
35	1225	40.0	452	2	US-09-773-877B-16	Sequence 16, Appl
36	1225	40.0	459	1	US-08-157-101A-7	Sequence 7, Appl
37	1225	40.0	462	2	US-09-773-877B-18	Sequence 18, Appl
38	1225	40.0	467	2	US-08-030-175-41	Sequence 41, Appl
39	1225	40.0	467	2	US-08-030-175-42	Sequence 42, Appl
40	1225	40.0	470	2	US-10-104-047-3730	Sequence 3730, Ap
41	1225	40.0	475	2	US-09-740-002-27	Sequence 27, Appl
42	1225	40.0	476	1	US-08-378-939-10	Sequence 10, Appl
43	1225	40.0	476	2	US-08-487-550-4	Sequence 4, Appl
44	1225	40.0	476	2	US-08-487-550-12	Sequence 12, Appl
45	1225	40.0	476	2	US-09-526-098-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-401-636-1  
; Sequence 1, Application US/09401636  
; Patent No. 6913749  
; GENERAL INFORMATION:  
; APPLICANT: Hellman, Lars T.  
; TITLE OF INVENTION: ENHANCED VACCINES  
; FILE REFERENCE: 10223/006001  
; CURRENT APPLICATION NUMBER: US/09/401.636  
; CURRENT FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: US 60/106,652  
; PRIOR FILING DATE: 1998-11-02  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-1

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Best Local Similarity	100.0%	Pred. No. 2e-136;		
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			Indels	0;
Gaps				0;
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QY	310	GELASTQSELTLSQKHWLSDRYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPDP	369	
Db	72	GELASTQSELTLSQKHWLSDRYTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPDP	131	
QY	370	LFIRKSPITCLVVDLAPSKGTNLTWRSRASKPVNHSRKEEKORNGTLTVTSTLPVGT	429	
Db	132	LFIRKSPITCLVVDLAPSKGTNLTWRSRASKPVNHSRKEEKORNGTLTVTSTLPVGT	191	
QY	430	RDWTEGYQCRVTHPHLPALMRSTTKTSQPRAAPEVYAFATPEWPGSRDKRTLAQLIQ	489	
Db	192	RDWTEGYQCRVTHPHLPALMRSTTKTSQPRAAPEVYAFATPEWPGSRDKRTLAQLIQ	251	
QY	490	NFMPEDISVQWMLHNEVQLPDARHSTQPRKTKGSGFFVFSRLEVTRAWEQKDEFTICRAV	549	
Db	252	NFMPEDISVQWMLHNEVQLPDARHSTQPRKTKGSGFFVFSRLEVTRAWEQKDEFTICRAV	311	
QY	550	HEAASPQTQRAVSVNPGK	569	
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RESULT 2
US-09-701-623C-1
; Sequence 1, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 325
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: CH2CH3 of human IgE
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
US-09-701-623C-1

Query Match 55.6%; Score 1701; DB 2; Length 325;
Best Local Similarity 99.4%; Pred. No. 6.2e-136;
Matches 318; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 310 GELASTQSELTLSQKHWLSDRTVTCQVYQHTFEDSTKCCADSNPRGVSAYLSRSPFD 369
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QY 550 HEAASPSQTVQRAVSNVPGK 569
DB 306 HEAASPSQTVQRAVSNVPGK 325

RESULT 3
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B

us-09-701-623C-1
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
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; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match 41.6%; Score 1273.5; DB 2; Length 711;
Best Local Similarity 50.1%; Pred. No. 3.5e-99;
Matches 286; Conservative 45; Mismatches 109; Indels 131; Gaps 16;

QY 1 EPKSCDKHTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 60
DB 236 EPKSCDKHTHTCPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 295

QY 61 NNYVDGVEVHNKTKPRREQYNSTYRVSVLTVTHQNMNGKEYKKCKVSKKALPAPIEKT 120
DB 296 NNYVDGVEVHNKTKPRREQYNSTYRVSVLTVTHQNMNGKEYKKCKVSKKALPAPIEKT 355

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVESNGQPENNYKTTTP 180
DB 356 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVESNGQPENNYKTTTP 415

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGKL----- 468
DB 416 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGKL----- 468

QY 241 GGGSGGGSGFTPTVKILQSSCD-----GGGHPPTIQLCLVSGYTPGINTIWLBD----- 293
DB 469 -----GGGS-----QVQLVQSGSELKKPGA-----SVKISKASGYTFTDYGMMVWKQAPG 514

QY 294 -----GQVMDVD-----LSTASTTQCEGELASTQSELTLSQKHWLSDRT 331
DB 515 QGLKMGWINTVTGASTYVDDFKGPFVSLDTSVSAAYLQISLKAEDT-----AT 565

QY 332 YTC-----QVYQHTFEDSTKCCADSNPRGVSAYLSRSPFDLFIKSPFITCLVVDL 385
DB 566 YFCARRGFVAMYWG-----QGTIVTVSSGGGGGGGGGGSDIVLTQSPA----- 613

QY 386 AFSGKGTVNLWTSRASKGPKVNHSTRKEEKQKNGTLTVTSTLPVTRDWISGETYQCRVTHP 445
DB 614 -----TMSASPGERV-----TLTCSASSISYMFYWHQRPGQS----- 646

QY 446 HLPALMRSTTK-TSGPRAAPEVYAFATPEWPGSRDKRTLACLIQFMFEDISVQWLNE 504
DB 647 --PRLLIYDTSNLASGVA-----RFGSGSGTSYSLTISRMEFEDATFYCHQS 694

QY 505 VOLPDARHSTTQPRKTGSGFPVFSRLVTR 535
DB 695 SSVP-----FTFGQ-----TKLEIKR 711

RESULT 4
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
```



APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/09/428,082B  
CURRENT FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 22  
LENGTH: 277  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fc-EMP-EMP  
US-09-428-082B-22

Query Match 40.6%; Score 1247; DB 2; Length 277;  
Best Local Similarity 81.8%; Pred. No. 1.5e-97;  
Matches 239; Conservative 7; Mismatches 12; Indels 34; Gaps 5;

Qy 6 DKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65  
Db 2 DKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Qy 66 GVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIETISKAK 125  
Db 62 GVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIETISKAK 121  
Qy 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 185  
Db 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181  
Qy 186 VGSFPLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSPGK 240  
Db 182 DGSFPLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSPGK 239  
Qy 241 -----GGSGGGSGFTPTPTVKILQSSCDGGGHFPPTIQLLCLVSG 280  
Db 240 HFGPLTWCKPQGGGGGGGTY-----SC-----HFGP-LTWCKPQ 276

RESULT 6  
US-09-428-082B-8  
Sequence 8, Application US/09428082B  
Patent No. 6660843  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/09/428,082B  
CURRENT FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 8  
LENGTH: 268  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fc-TMP-TMP  
US-09-428-082B-8

Query Match 40.6%; Score 1243; DB 2; Length 268;  
Best Local Similarity 88.9%; Pred. No. 3.2e-97;  
Matches 232; Conservative 5; Mismatches 14; Indels 10; Gaps 1;

Qy 6 DKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65

CURRENT APPLICATION NUMBER: US/10/071,485  
CURRENT FILING DATE: 2002-02-07  
PRIOR APPLICATION NUMBER: 09/485,737  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 90  
LENGTH: 711  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-10-071-485-90

Query Match 41.6%; Score 1273.5; DB 2; Length 711;  
Best Local Similarity 50.1%; Pred. No. 3.5e-99;  
Matches 286; Conservative 45; Mismatches 109; Indels 131; Gaps 16;

Qy 1 EPKSCDKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 236 EPKSCDKTHCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 295  
Qy 61 NWYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIET 120  
Db 296 NWYVDGVEVHNKTPREBQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIET 355  
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 180  
Db 356 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 415  
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSPGK 240  
Db 416 PVLDSVGSFPLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTQKLSLSPGK 468  
Qy 241 GGGSGGGSGFTPTPTVKILQSSCD-----GGGHFPPTIQLLCLVSGYTPGTINITWLED--- 293  
Db 469 -----GGSG-----QVQLVQSGSELKPKGA-----SVKISCKASGYTFTDYGMWVWQAPG 514  
Qy 294 -----GQVMDVD-----LSTASTTQEGELASTQSELTLSQKHLSDRT 331  
Db 515 QQLKMWGINTVGTSTVYDPPKGRFVFLDTLSVSAAYLQISLKAEDT-----AT 565  
Qy 332 YTC-----QVYQGHTEFSDTKKCADSNPRGVSAYLRSPFDLFIKSPITITCLVVDL 385  
Db 566 YFCARRGYAMYDWG-----QGTFTVTVSSGGSGGGGGGGSDIVLTQSPA----- 613  
Qy 386 APSKGTVNLTVSRASGKPVNSTRKEKQRNGLTTLVPTVGTDRDWIEGETYQCRVTHP 445  
Db 614 -----TWASGGERV-----TLTCSASSISYFMFWHQRPQS----- 646  
Qy 446 HLPALRMSTTK-TSGPRAAPEVYAPATPWPGRDKRTLACLIONFMPEDISVOWHLNE 504  
Db 647 --PRLIYDTSNLASGVEA-----RFGSGSGTSYSLSITSRMEPEDFATYFCHQS 694  
Qy 505 VOLPARHSTTPRKTSGSPFVSRLEVTR 535  
Db 695 SSYP-----FTFGQ-----TKLEIKR 711

RESULT 5  
US-09-428-082B-22  
Sequence 22, Application US/09428082B  
Patent No. 6660843  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: CHEETHAM, JANET C.

Db 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Qy 66 GVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMMGKEYKCKVSNKALPAPIEKTISKAK 125  
Db 62 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPIEKTISKAK 121  
Qy 126 VQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 185  
Db 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181  
Qy 186 VGSFFLYSKLTVDKSRWQOQGVFSCSVMHREALHNNHYQORSLSPGKVEGGSGG---- 240  
Db 182 DGSFFLYSKLTVDKSRWQOQGVFSCSVMHREALHNNHYQORSLSPGKVEGGSGGEGPTLRQ 241  
Qy 241 -----GGGGGGGGFTPTTVK 256  
Db 242 WLAARAGGGGGGIEGPTLR 262

## RESULT 7

US-09-422-838C-46  
; Sequence 46, Application US/09422838C  
; Patent No. 6835809  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Chuan-Fa  
; APPLICANT: Feige, Ulrich  
; APPLICANT: Cheetham, Janet C.  
; TITLE OF INVENTION: Thrombopoietic Compounds  
; FILE REFERENCE: 01017/36263  
; CURRENT APPLICATION NUMBER: US/09/422,838C  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,348  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-422-838C-46

Query Match 40.6%; Score 1243; DB 2; Length 269;  
Best Local Similarity 88.9%; Pred. No. 3.2e-97;  
Matches 232; Conservative 5; Mismatches 14; Indels 10; Gaps 1;

Qy 6 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65  
Db 2 DKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 61  
Qy 66 GVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMMGKEYKCKVSNKALPAPIEKTISKAK 125  
Db 62 GVEVHNKTKPREEQNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPIEKTISKAK 121  
Qy 126 VQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 185  
Db 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 181  
Qy 186 VGSFFLYSKLTVDKSRWQOQGVFSCSVMHREALHNNHYQORSLSPGKVEGGSGG---- 240  
Db 182 DGSFFLYSKLTVDKSRWQOQGVFSCSVMHREALHNNHYQORSLSPGKVEGGSGGEGPTLRQ 241  
Qy 241 -----GGGGGGGGFTPTTVK 256  
Db 242 WLAARAGGGGGGIEGPTLR 262

## RESULT 8

US-09-181-706-8  
; Sequence 8, Application US/09181706  
; Patent No. 6130068  
; GENERAL INFORMATION:

; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
; APPLICANT: Robert F. DuBoise, Richard S. Johnson  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,706  
; FILING DATE: October 28, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/958,598 (converted to a  
; APPLICATION NUMBER: Provisional, see below)  
; FILING DATE: October 28, 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598  
; APPLICATION NUMBER: conversion to Provisional application)  
; FILING DATE: October 26, 1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 660 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-181-706-8

Query Match 40.3%; Score 1232; DB 2; Length 660;  
Best Local Similarity 93.0%; Pred. No. 1e-95;  
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 32 DKRSCDKTHTCPPCAPPEAEGAPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 91  
Qy 61 NNYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMMGKEYKCKVSNKALPAPIEKT 120  
Db 92 NNYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPIEKT 151  
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180  
Db 152 ISKAKQPREPOVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 211  
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQOQGVFSCSVMHREALHNNHYQORSLSPGKVEGGSGG 240  
Db 212 PVLDSGDSFFLYSKLTVDKSRWQOQGVFSCSVMHREALHNNHYQORSLSPGK--GGGGSG 269  
Qy 241 GGS 244  
Db 270 GGS 273

## RESULT 9

US-09-458-791-8

```

; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-066-8

Query Match 40.3%; Score 1232; DB 2; Length 660;
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 227; Conservative 7; Mismatches 8; Indels 2; Gaps 1

QY 1 EPKSCDTHTCPCPAPELLGGPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 32 DKRSCDTHTCPCPAPEAGAPSVFLFPPPKDTHLMISRTPEVTCVVVDVSHEDPEVKF 91
QY 61 NWTVDGVEVHNVTCKPREEQNSTYRVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
DB 92 NWTVDGVEVHNATCKPREEQNSTYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 151
QY 121 ISKAKVQPREPQVYTLPPSRDELTKQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTP 180
DB 152 ISKAKGQPREPQVYTLPPSREEMTKQVSLTCLVKGPYPSDIAVEWESNGQPENNYKTTP 211
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFCSVMHAEALHNHYQOBSLSISPGKVGSGGSG 240
DB 212 PVLDSVGSFPLYSKLTVDKSRWQGNVFCSSVMHEALHNHYTKQSLSLSPGK--GGGSG 269
QY 241 GGGG 244
DB 270 GGGG 273

RESULT 11
US-09-459-065-8
; Sequence 8, Application US/09459065
; Patent No. 6562949
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry

```

```

; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,065
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-065-8

Query Match 40.3%; Score 1232; DB 2; Length 660;
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 22; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 32 DKRSCDKTHTCPCPAPEAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 91
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 92 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 151
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 152 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 211
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCSVHREALHNNHYQORSLSLSPGKV 240
Db 212 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVHREALHNNHYTKQSLSPGK--GGGGG 269
QY 241 GGGG 244
Db 270 GGGG 273

RESULT 12
US-10-679-999-9
; Sequence 9, Application US/10679999
; Patent No. 6936439
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA

; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,065
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-065-8

Query Match 40.3%; Score 1232; DB 2; Length 660;
Best Local Similarity 93.0%; Pred. No. 1e-95;
Matches 22; Conservative 7; Mismatches 8; Indels 2; Gaps 1;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 32 DKRSCDKTHTCPCPAPEAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 91
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 92 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 151
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 152 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 211
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCSVHREALHNNHYQORSLSLSPGKV 240
Db 212 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVHREALHNNHYTKQSLSPGK--GGGGG 269
QY 241 GGGG 244
Db 270 GGGG 273

RESULT 13
US-09-428-082B-16
; Sequence 16, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHESTNAN, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 253

; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1
; OTHER INFORMATION: /note= "Met (ATG) starts at -1"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-679-999-9

Query Match 40.2%; Score 1229; DB 2; Length 379;
Best Local Similarity 97.0%; Pred. No. 8.2e-96;
Matches 226; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 2 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 61
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 62 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 121
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 122 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 181
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCSVHREALHNNHYQORSLSLSPGKV 233
Db 182 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVHREALHNNHYTKQSLSPGKV 234
```

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fc-EMP  
US-09-428-082B-16

Query Match 40.1%; Score 1226; DB 2; Length 253;  
Best Local Similarity 84.7%; Pred. No. 8.1e-96;  
Matches 233; Conservative 7; Mismatches 11; Indels 24; Gaps 4;

Qy 6 DKHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 65  
Db 2 DKHTCPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 61

Qy 66 GVEVHNKTKPREQYNSTYRVVSVLTVLHQWMNKGKEYCKVSNKALPAPIET 125  
Db 62 GVEVHNKTKPREQYNSTYRVVSVLTVLHQWMNKGKEYCKVSNKALPAPIET 121

Qy 126 VQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 185  
Db 122 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 181

Qy 186 VGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 245  
Db 182 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232

Qy 246 GGSFTPTVKILOSSCGGHHFPPTIQLCLIVSG 280  
Db 233 GGGTY-----SC----HFGP-LTWCKPQG 252

RESULT 14  
US-08-595-043A-50  
Sequence 50, Application US/08595043A  
Patent No. 5915824

GENERAL INFORMATION:  
APPLICANT: SGARLATO, GREGORY D.  
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/595,043A  
FILING DATE: 31-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: SGAR-00371  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-595-043A-50

Query Match 40.0%; Score 1225; DB 1; Length 232;  
Best Local Similarity 97.0%; Pred. No. 8.7e-96;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQWMNKGKEYCKVSNKALPAPIET 120  
Db 61 NWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQWMNKGKEYCKVSNKALPAPIET 120

Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232  
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232

RESULT 15  
US-09-968-362A-26  
Sequence 26, Application US/09968362A  
Patent No. 6797493

GENERAL INFORMATION:  
APPLICANT: Sun, Lee-Hwei K  
APPLICANT: Sun, Bill  
APPLICANT: Sun, Cecily R  
TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
TITLE OF INVENTION: increased biological activities  
FILE REFERENCE: 035UN2001  
CURRENT APPLICATION NUMBER: US/09/968,362A  
CURRENT FILING DATE: 2001-10-01  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 26  
LENGTH: 232  
TYPE: PRT  
ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
US-09-968-362A-26

Query Match 40.0%; Score 1225; DB 2; Length 232;  
Best Local Similarity 97.0%; Pred. No. 8.7e-96;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Qy 61 NWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQWMNKGKEYCKVSNKALPAPIET 120  
Db 61 NWYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQWMNKGKEYCKVSNKALPAPIET 120

Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232  
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232

Search completed: November 30, 2005, 00:34:04  
Job time : 46 secs

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